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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 90.8333 Seconds  
(without alignments)  
464.112 Million cell updates/sec

Title: US-09-674-857-1  
Perfect score: 581  
Sequence: 1 APPVAGPSVLPFPKPKDYL.....CKVSNKGLPSSIBKTIISKAK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	109	3	AAY54996 Mutated C
2	567	97.6	449	6	AEE37576 Human FD1
3	565	97.2	462	2	AAW14933 2A2 (Chim
4	565	97.2	462	2	AAW14934 2A2 (Chim
5	565	97.2	463	2	AAW14939 3F4 (Chim
6	565	97.2	463	2	AAW14940 3F4 (Chim
7	565	97.2	472	5	ABP51695 SGL.1-TPO
8	565	97.2	472	8	ADQ16647 Immunoglo
9	562	96.7	326	8	ADF77155 Anti-VAP-
10	562	96.7	447	8	ADQ17121 Humanised
11	562	96.7	462	8	ADF77154 Chimeric
12	559.5	96.3	110	3	AAY54998 Mutated C
13	559	96.2	436	7	ADM33853 Human HuE
14	559	96.2	436	8	ADR48984 HuBPO-L-F
15	559	96.2	448	7	ADM33376 Human GCS
16	554	95.4	109	2	AAR41709 Undefined
17	554	95.4	109	3	AAY54997 Mutated C
18	554	95.4	217	3	AB07476 Amino aci
19	554	95.4	217	4	AB76423 Human IGG
20	554	95.4	217	4	AAB76203 Human IGG
21	554	95.4	217	5	AAG78434 Native se
22	554	95.4	217	6	ABR42440 Human IGG
23	554	95.4	217	8	ADH75378 Human IGG
24	554	95.4	228	5	ABG31095 Human mat
25	554	95.4	228	8	ADR48993 Human IGG

26	554	95.4	310	8	ADS84436 Human ant
27	554	95.4	310	8	ADR68578 Human ant
28	554	95.4	326	4	AAE02643 Human imm
29	554	95.4	326	5	AAM47857 Human IGF-
30	554	95.4	326	5	ABG30462 Human ant
31	554	95.4	326	5	ABG77148 Anti-IGF-
32	554	95.4	326	6	AAE32916 Human imm
33	554	95.4	326	6	AAE32628 Human imm
34	554	95.4	326	6	AAO30894 Human IGG
35	554	95.4	326	7	ADE97353 Human IGG
36	554	95.4	326	7	ADF75002 Human IGF
37	554	95.4	326	8	ADM41541 Anti-Inte
38	554	95.4	326	8	ADQ95469 Human IGG
39	554	95.4	326	8	ADR28562 Human ant
40	554	95.4	381	2	AAY06895 Human IL-
41	554	95.4	432	2	AAR26782 CD4-gamma
42	554	95.4	432	2	AAR46678 CD4-gamma
43	554	95.4	432	3	AAY85079 Human CD4
44	554	95.4	432	4	AAB67322 CD4-gamma
45	554	95.4	432	4	AAB80883 Human CD4

ALIGNMENTS

RESULT 1  
AAY54996  
ID AAY54996 standard; protein; 109 AA.

XX AC AAY54996;

XX DT 17-FEB-2000 (first entry)

XX DE Mutated CH2 sequence G1deltaaab.

XX KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIB;  
cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
Crohn's disease; graft-vs-host disease; organ transplant rejection;  
bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
allotransplant rejection; autoimmune haemolytic anaemia; inflammatory disease;  
autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
sickle cell anaemia; coronary artery occlusion.

XX OS Synthetic.

XX PN W0958572-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001441.

XX PR 08-MAY-1998; 98GB-00009951.

XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PI Armour KL, Clark MR, Williamson LM;

XX WPI; 2000-039075/03.

XX PT Immunoglobulin-derived binding molecules that do not activate complement  
or trigger cytotoxic activities and maintaining desirable immunoglobulin  
properties.

XX PS Claim 12; Fig 17; 81pp; English.

XX CC This sequence represents the mutated CH2 molecule G1deltaab, and is a  
binding molecule of the invention. The recombinant binding molecule is  
capable of binding a target molecule without triggering complement  
dependent lysis, or the cell-mediated destruction of the target  
comprises: (a) a binding domain capable of binding a target molecule; and  
(b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
 CC molecule is used to bind a target molecule (especially FcγγmαRIIb  
 CC causing inhibition of B cell activation, mast cell degranulation or  
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
 CC binding of a second binding molecule, e.g. an antibody, to the target  
 CC molecule. The binding molecule is useful for the treatment of graft-vs-  
 CC host disease, organ transplant rejection, bone-marrow transplant  
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
 CC foetal/neonatal alloimmune thrombocytopenia and arthritis), alloimmunity (e.g.  
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
 CC coronary artery occlusion). The binding molecules do not activate  
 CC complement or trigger cytotoxic activities through Fcγγmαr and desirable  
 CC IgG properties have been retained. The polypeptides do not contain non-  
 CC human amino acids, and are therefore likely to have reduced  
 CC immunogenicity. Further, they still bind Protein A, which is consistent  
 CC with being able to cross the human placenta through interaction with FcRn  
 CC (neonatal Fc receptor)  
 XX  
 SQ Sequence 109 AA;

Query Match 100.0%; Score 581; DB 3; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-52;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 |||||  
 DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 |||||  
 QY 61 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSKNKGSLPSSIEKTSKAK 109  
 |||||  
 DB 61 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSKNKGSLPSSIEKTSKAK 109  
 |||||

RESULT 2  
 AAE37576  
 ID AAE37576 standard; protein; 449 AA.  
 AC AAE37576;  
 XX  
 XX 27-AUG-2003 (first entry)  
 DE Human FDI2-Ig alphatp fusion protein variant.  
 XX  
 XX Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;  
 KW human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; DI;  
 KW D2; alpha tailpiece; alphatp; fusion protein; mutein; variant; mutant.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 218 /note= "Wild type Glu substituted with Pro"  
 FT Misc-difference 219 /note= "Wild type Leu substituted with Val"  
 FT Misc-difference 221 /note= "Wild type Gly substituted with Ala"  
 XX  
 XX W02003040311-A2.  
 PN  
 XX  
 XX 15-MAY-2003.  
 PD  
 XX  
 XX 24-OCT-2002; 2002WO-US034393.  
 PF  
 XX  
 XX 25-OCT-2001; 2001US-0346231P.  
 PR  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX  
 XX Arthos J, Cicala C, Fauci AS;  
 PI  
 XX  
 XX WPI; 2003-441545/41.  
 DR  
 DR N-PSDB; ACC82877.

XX New CD4 polypeptide ligated at its C-terminus with a portion of an  
 PT immunoglobulin, useful for preparing a composition for treating or  
 PT preventing HIV-1 infection.  
 XX  
 XX Example 11; Page 67; 100pp; English.  
 PS  
 XX The invention relates to a CD4 (cluster of differentiation factor 4)  
 CC polypeptide ligated at its C-terminus with a portion of an immunoglobulin  
 CC (Ig) comprising a hinge region and a constant domain of a mammalian Ig  
 CC heavy chain. The polypeptide comprises a tailpiece from the C-terminus of  
 CC the heavy chain of an IGA or IGM antibody. Polypeptides of the invention  
 CC are useful for preparing a composition for treating or preventing human  
 CC immunodeficiency virus (HIV)-1 infection. The invention is useful in gene  
 CC therapy and also in the preparation of vaccines. The present sequence is  
 CC a fusion protein variant (G218P/L219V/220delA/G221A) which comprises a  
 CC human IGA alpha tailpiece (alphatp), a human IGG2 constant region  
 CC comprising a hinge, a CH2 and CH3 region and a human CD4 D1D2 domain.  
 CC This variant protein is also referred to as mutant F  
 XX  
 SQ Sequence 449 AA;

Query Match 97.6%; Score 567; DB 6; Length 449;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-49;  
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 |||||  
 DB 216 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 275  
 |||||  
 QY 61 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSKNKGSLPSSIEKTSKAK 109  
 |||||  
 DB 276 REEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSKNKGSLPSSIEKTSKAK 324  
 |||||

RESULT 3  
 AAW14933  
 ID AAW14933 standard; protein; 462 AA.  
 AC AAW14933;  
 XX  
 XX 17-OCT-2003 (revised)  
 DT 16-JUN-1997 (first entry)  
 XX  
 XX 2A2 (Chimeric) human G2/G4 chimeric antibody.  
 XX  
 XX Xenotransplantation; graft rejection; cell interaction; pig;  
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
 KW chimeric antibody; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS Mus sp.  
 OS Chimeric.  
 XX  
 XX W09711971-A1.  
 PN  
 XX  
 XX 03-APR-1997.  
 PD  
 XX  
 XX 27-SEP-1996; 96WO-US015575.  
 PF  
 XX  
 XX 28-SEP-1995; 95US-0004489P.  
 PR 26-SEP-1996; 96US-00004489.  
 XX  
 XX (ALEX-) ALEXION PHARM INC.  
 PA  
 XX  
 XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;  
 PI  
 XX  
 XX WPI; 1997-212855/19.  
 DR N-PSDB; AAT62931.  
 DR  
 XX Antibodies binding to porcine but not human cell interaction proteins -  
 PT useful to treat and assay for rejection of xenografted porcine organs,  
 PT tissues or cells.



Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 DB 248 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 307  
 QY 61 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109  
 DB 308 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 356

RESULT 6  
 AAW14940  
 ID AAW14940 standard; protein; 463 AA.  
 AC AAW14940;  
 XX 17-OCT-2003 (revised)  
 DT 16-JUN-1997 (first entry)  
 XX 3F4 (Chimeric) human G2/G4 chimeric antibody.  
 DE XX  
 KW Xenotransplantation; graft rejection; cell interaction; pig;  
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
 KW chimeric antibody; diagnosis.  
 XX Homo; sapiens.  
 OS Mus sp.  
 OS Chimeric.  
 XX WO9711971-A1.  
 XX 03-APR-1997.  
 XX 27-SEP-1996; 96WO-US015575.  
 XX 28-SEP-1995; 95US-0004489P.  
 XX 26-SEP-1996; 96US-00004489.  
 XX (ALEX-) ALEXION PHARM INC.  
 XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;  
 XX WPI; 1997-212855/19.  
 XX N-PSDB; AAT62937.  
 XX Antibodies binding to porcine but not human cell interaction proteins -  
 PT useful to treat and assay for rejection of xenografted porcine organs,  
 PT tissues or cells.  
 XX Disclosure; Page 58-61; 105pp; English.

XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of  
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a  
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)  
 CC monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see  
 CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is  
 CC useful for diagnosing human rejection of porcine xenotransplants and for  
 CC improving xenotransplantation of porcine cells, tissues and organs into  
 CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 463 AA;

Query Match 97.2%; Score 565; DB 2; Length 463;  
 Best Local Similarity 97.2%; Pred. No. 1.9e-49;  
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 DB 248 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 307  
 QY 61 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109  
 DB 308 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 356

DB 308 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 356

RESULT 7  
 ABP51695  
 ID ABP51695 standard; protein; 472 AA.  
 AC ABP51695;  
 XX 01-OCT-2002 (first entry)  
 DT  
 XX SG1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.  
 DE  
 XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;  
 KW complementarity determining region; immunoglobulin; antianaemic;  
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS WO200246238-A2.  
 XX 13-JUN-2002.  
 XX 05-DEC-2001; 2001WO-US047656.  
 XX 05-DEC-2000; 2000US-0251448P.  
 XX 04-MAY-2001; 2001US-0288889P.  
 XX 29-MAY-2001; 2001US-0294068P.  
 XX (ALEX-) ALEXION PHARM INC.  
 XX Bowdish KS, Barbas-Frederickson S, Renshaw M;  
 XX WPI; 2002-566610/60.  
 XX N-PSDB; ABQ73374.

XX A novel immunogen molecule comprising a region in which amino acid  
 PT residues corresponding to at least a portion of the complementary  
 PT determining region are replaced or fused with an erythropoietin or  
 PT thrombopoietin mimetic.  
 XX Example 4; Fig 13A; 113pp; English.  
 XX The present invention describes an immunoglobulin molecule or its fragment  
 CC (I) comprising a region where amino acid residues corresponding to at  
 CC least a portion of the complementary determining region (CDR) are  
 CC replaced or fused with biologically active peptides e.g. a peptide  
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,  
 CC that is flanked with proline at its carboxy terminus. (I) has  
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as  
 CC a stimulator of proliferation, differentiation and maturation of  
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful  
 CC for stimulating proliferation, differentiation or growth of  
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with  
 CC production (I) with a region where amino acid residues corresponding to  
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or  
 CC more of its CDRs fused to an EPO mimetic. (I) is useful for increasing the  
 CC production of red blood cells, where (I) is contacted with haematopoietic  
 CC stem cells or their progenitors. (I) is useful for diagnostics or  
 CC therapeutics, in cell isolation strategies, and for treating patients  
 CC suffering from deficiency in cell populations caused by disease,  
 CC disorders or treatments related to the suppression of haematopoiesis.  
 CC ABQ73288 to ABQ73377 and ABP51695 to ABP51696 represent sequences used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 472 AA;

Query Match 97.2%; Score 565; DB 5; Length 472;  
 Best Local Similarity 97.2%; Pred. No. 2e-49;  
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;



QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 Db 257 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316  
 QY 61 REEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109  
 Db 317 REEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 365

RESULT 8  
 ADQ16647  
 ID ADQ16647 standard; protein; 472 AA.  
 XX AC ADQ16647;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Immunoglobulin antibody 5G1.1-TPO heavy chain SEQ ID NO:67.  
 XX KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;  
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;  
 KW immunotherapy; thrombocytopenia.  
 XX OS Synthetic.  
 XX PN W02004050017-A2.  
 XX PD 17-JUN-2004.  
 XX PF 17-NOV-2003; 2003WO-US036894.  
 XX PR 02-DEC-2002; 2002US-00307724.  
 XX PA (ALEX-) ALEXION PHARM INC.  
 XX PI Bowdish KS, Frederickson S, Renshaw M;  
 XX WPI; 2004-460973/43.  
 DR N-PSDB; ADQ16648.  
 XX PT New immunoglobulin molecule comprising a region, where two  
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic  
 PT or a TPO mimetic, useful for treating thrombocytopenia.  
 XX Example 4; SEQ ID NO 67; 107pp; English.  
 XX CC The invention relates to a novel immunoglobulin molecule or its fragment  
 CC comprising a region where amino acid residues corresponding to at least a  
 CC portion of a two complementarity determining regions (CDRs) are replaced  
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and  
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the  
 CC invention has immunosuppressive activity, and may have a use in  
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or  
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow  
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.  
 CC The present sequence represents an immunoglobulin antibody heavy chain of  
 CC the invention.  
 XX Sequence 472 AA;  
 Query Match 97.2%; Score 565; DB 8; Length 472;  
 Best Local Similarity 97.2%; Pred. No. 2e-49;  
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 Db 257 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316  
 QY 61 REEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109  
 Db 317 REEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 365

us-09-674-857-1.rag

RESULT 9  
 ADF77155  
 ID ADF77155 standard; protein; 326 AA.  
 XX AC ADF77155;  
 XX DT 26-FEB-2004 (first entry)  
 XX DE Anti-VAP-1 monoclonal antibody H chain constant region.  
 XX KW complementarity determining region; CDR; mouse;  
 KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;  
 KW chimeric; inflammatory disorder; rheumatoid arthritis;  
 KW inflammatory bowel disease; autoimmune disease; psoriasis;  
 KW immunosclerotic imaging.  
 XX OS Homo sapiens.  
 XX PN W02003093319-A1.  
 XX PD 13-NOV-2003.  
 XX PF 28-APR-2003; 2003WO-FI000330.  
 XX PR 29-APR-2002; 2002FI-00000807.  
 XX PA (BIOT-) BIOTIE THERAPIES CORP.  
 XX PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;  
 XX WPI; 2004-022642/02.  
 XX PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and  
 PT encoding nucleic acid molecules, useful for diagnosing and treating  
 PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.  
 XX Claim 18; SEQ ID NO 16; 56pp; English.  
 XX CC This sequence represents the constant region of a human anti-Vascular  
 CC Adhesion Protein-1 (VAP-1) antibody heavy chain. This sequence may be  
 CC used in the production of a chimeric mouse-human anti-VAP-1 antibody. The  
 CC nucleic acid molecules, polypeptides or antibodies are useful in treating  
 CC VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis,  
 CC inflammatory bowel disease, autoimmune diseases or psoriasis. The  
 CC chimeric VAP-1 antibody is further used for in vitro and in vivo  
 CC diagnostic applications, including in vivo immunosclerotic imaging of  
 CC inflammation sites. The chimeric MAb's of the invention have improved  
 CC kinetic properties compared to the corresponding murine antibodies.  
 XX Sequence 326 AA;  
 Query Match 96.7%; Score 562; DB 8; Length 326;  
 Best Local Similarity 95.4%; Pred. No. 2.6e-49;  
 Matches 104; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 Db 111 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170  
 QY 61 REEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109  
 Db 171 REEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 219

RESULT 10  
 ADQ17121  
 ID ADQ17121 standard; protein; 447 AA.  
 XX AC ADQ17121;  
 XX DT 07-OCT-2004 (first entry)  
 XX DE Humanised anti-NGF antibody E3 heavy chain full-length protein.



Query Match 96.7%; Score 562; DB 8; Length 462;  
 Best Local Similarity 95.4%; Pred. No. 4e-49;  
 Matches 104; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 DB 247 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 306

QY 61 REEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109  
 DB 307 REEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 355

RESULT 12  
 AAY54998  
 ID AAY54998 standard; protein; 110 AA.  
 XX AC AAY54998;  
 XX  
 DT 17-FEB-2000 (first entry)  
 DE DE  
 XX Mutated CH2 sequence Gidelataac.  
 XX  
 KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;  
 KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
 KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
 KW sickle cell anaemia; coronary artery occlusion.  
 XX  
 OS Synthetic.  
 PN WO9958572-A1.  
 XX  
 XX 18-NOV-1999.  
 XX  
 XX 07-MAY-1999; 99WO-GB001441.  
 XX  
 XX 08-MAY-1998; 98GB-00009951.  
 XX  
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
 XX  
 XX Armour XL, Clark MR, Williamson LM;  
 XX  
 XX WPI; 2000-039075/03.  
 XX  
 XX Immunoglobulin-derived binding molecules that do not activate complement  
 PT or trigger cytotoxic activities and maintaining desirable immunoglobulin  
 PT properties.  
 XX  
 XX Claim 12; Fig 17; 81pp; English.  
 XX  
 XX This sequence represents the mutated CH2 molecule Gidelataac, and is a  
 CC binding molecule of the invention. The recombinant binding molecule is  
 CC capable of binding a target molecule without triggering complement  
 CC dependent lysis, or the cell-mediated destruction of the target  
 CC comprises: (a) a binding domain capable of binding a target molecule; and  
 CC (b) an effector domain that is homologous to all or part of a constant  
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
 CC molecule is used to bind a target molecule (especially FcgammaRIIb  
 CC causing inhibition of B cell activation, mast cell degranulation or  
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
 CC binding of a second binding molecule, e.g. an antibody, to the target  
 CC molecule. The binding molecule is useful for the treatment of graft-vs-  
 CC host disease, organ transplant rejection, bone-marrow transplant  
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
 CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.  
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and

CC coronary artery occlusion). The binding molecules do not activate  
 CC complement or trigger cytotoxic activities through FcgammaR and desirable  
 CC IgG properties have been retained. The polypeptides do not contain non-  
 CC human amino acids, and are therefore likely to have reduced  
 CC immunogenicity. Further, they still bind Protein A, which is consistent  
 CC with being able to cross the human placenta through interaction with FcRn  
 CC (neonatal Fc receptor)

SQ Sequence 110 AA;  
 Query Match 96.3%; Score 559.5; DB 3; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 1.2e-49;  
 Matches 108; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59  
 DB 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 60 PREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109  
 DB 61 PREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 13  
 ADM33853  
 ID ADM33853 standard; protein; 436 AA.  
 XX AC ADM33853;  
 XX  
 DT 03-JUN-2004 (first entry)  
 DE DE  
 XX Human HuEPO-L-VFcgamma2 fusion protein.  
 XX  
 KW Erythropoietin; EPO; immunoglobulin; IgG;  
 KW fragment crystallisation region; FC; chronic anaemia; renal disease;  
 KW cancer chemotherapy; rheumatoid arthritis; AIDS;  
 KW myelodysplastic syndrome; (HuEPO)-L-VFcgamma2; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PH Key  
 FT Peptide 1..27 Location/Qualifiers  
 FT Protein /note= "Signal peptide"  
 FT Peptide /note= "EPO"  
 FT Peptide 193..208  
 FT Protein /note= "Linker"  
 FT Protein 209..436  
 FT Misc-difference /note= "IgG2 Fc"  
 FT /note= "Wild-type Pro substituted by Ser"  
 XX  
 XX US2003082749-A1.  
 XX  
 XX 01-MAY-2003.  
 XX  
 XX 17-AUG-2001; 2001US-00932812.  
 XX  
 XX 17-AUG-2001; 2001US-00932812.  
 XX  
 XX (SUNL/) SUN L K.  
 XX (SUNB/) SUN B N C.  
 XX (SUNC/) SUN C R Y.  
 XX  
 XX Sun LK, Sun BNC, Sun CRY;  
 PI WPI; 2003-616080/58.  
 DR  
 XX New recombinant human erythropoietin-L-VFc fusion proteins, useful for  
 PT treating patients with chronic anemia caused by renal failure, cancer  
 PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV  
 PT infection.



```
QY 61 REEQNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTIKAK 109
Db 281 REEQNSTFRVSVLTVVHODWLNKGYKCKVSNKGLPASIETIKTK 329

RESULT 15
ADM33376
ID ADM33376 standard; protein; 448 AA.
XX AC ADM33376;
XX DT 03-JUN-2004 (first entry)
XX DE Human GCSF-L-fragment of crystallisation gamma 2 fusion protein.
XX cytotatic; immunostimulant; antianaemic; anti-HIV; protein therapy;
KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;
KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;
KW haematopoietic disorder; cancer; chemotherapy; leukaemia; AIDS;
KW bone marrow transplantation; chronic neutropenia; fusion protein;
KW fragment of crystallisation gamma 2; FC gamma 2.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .30
FT Protein /label= GCSF leader peptide
FT /note= "Mature human GCSF-L-fragment of crystallisation
FT gamma 2 fusion"
FT Misc-difference 331
FT /note= "Wild type Pro substituted by Ser"
XX
XX US2003082679-A1.
XX 01-MAY-2003.
XX 01-OCT-2001; 2001US-00968362.
XX 01-OCT-2001; 2001US-00968362.
XX (SUNL/) SUN L K.
XX (SUNB/) SUN B N C.
XX (SUNC/) SUN C R Y.
XX Sun LK, Sun BNC, Sun CRY;
XX WPI; 2003-585400/55.
XX N-PSDB; ADM33375.
XX
XX New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-
XX vFc fusion protein for treating immune or hematopoietic system disorders
XX comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G
XX FC variant.
XX Disclosure; Fig 2A; 15pp; English.
XX
XX The invention describes a recombinant human granulocyte colony-
XX stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a
XX peptide linker, and a human immunoglobulin G (IgG) FC variant. Also
XX described are: a CHO-derived cell line producing the above hG-CSF-L-vFc
XX fusion protein in its growth medium in excess of 10 µg/mg per million
XX cells in a 24-hour period; and making the recombinant fusion protein
XX cited above, comprising generating a CHO-derived cell line cited above,
XX growing the cell line under conditions the recombinant fusion protein is
XX expressed in its growth medium, and purifying the expressed protein. The
XX recombinant fusion protein is useful in treating a variety of conditions
XX associated with an impaired immune or haematopoietic system, including
XX cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow
XX transplantation, and chronic neutropenias. This is the amino acid
XX sequence of human GCSF-L-fragment of crystallisation gamma 2 variant
XX fusion protein.
XX
```

```
XX SQ Sequence 448 AA;
Query Match 96.2%; Score 559; DB 7; Length 448;
Best Local Similarity 94.5%; Pred. No. 7.8e-49;
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 APPVAGPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 233 APPVAGPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 292
QY 61 REEQNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTIKAK 109
Db 293 REEQNSTFRVSVLTVVHODWLNKGYKCKVSNKGLPASIETIKTK 341

Search completed: November 17, 2005, 07:04:53
Job time : 93.8333 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:49:37 ; Search time 17.9178 Seconds  
(without alignments)  
585.319 Million cell updates/sec

Title: US-09-674-857-1  
Perfect score: 581  
Sequence: 1 APPVAGPSVFLPPPKPDTL.....CKVSNKGLPSSIEKTISKAK 109  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	95.4	326	1 G2HU	Ig gamma-2 chain C
2	545	93.8	234	2 PT0207	Ig gamma chain C r
3	543	93.5	255	4 S31866	Ig gamma-1 chain C
4	543	93.5	330	1 GHUU	Ig gamma-1 chain C
5	543	93.5	374	2 S69339	Ig heavy chain V r
6	540	92.9	327	1 G4HU	Ig gamma-4 chain C
7	524	90.2	377	2 A23511	Ig gamma-3 chain C
8	524	90.2	377	2 A60764	Ig gamma-3 chain C
9	504	86.7	289	1 G3HUM1	Ig gamma-3 heavy c
10	458	78.8	328	2 I47160	Ig gamma 2b chain
11	458	78.8	328	2 I47159	Ig gamma 2a chain
12	453	78.0	277	2 I47162	Ig gamma 4 chain c
13	442	76.1	328	2 I47161	Ig gamma 3 chain c
14	442	76.1	328	2 I47158	Ig gamma 1 chain c
15	429	73.8	470	2 S22080	Ig heavy chain pre
16	420	72.3	333	2 PS0018	Ig gamma-2b chain
17	417	71.8	329	1 G2GP	Ig gamma-2 chain C
18	413	71.1	323	1 GHRB	Ig gamma chain C r
19	411	70.7	327	2 S06611	Ig gamma-2 chain C
20	410.5	70.7	329	1 G3MSC	Ig gamma-3 chain C
21	410.5	70.7	398	1 G3MSM	Ig gamma-3 chain C
22	410	70.6	308	2 C30554	Ig heavy chain C r
23	410	70.6	472	2 C31459	Ig gamma-1 chain -
24	396	68.2	324	1 G1MS	Ig gamma-1 chain C
25	396	68.2	393	1 G1MSM	Ig gamma-1 chain C
26	396	68.2	444	2 PC4436	monoclonal antibod
27	392	67.5	329	2 S00847	Ig gamma-2c chain
28	382	65.7	335	1 G2MSAB	Ig gamma-2a chain
29	382	65.7	405	1 G2MSBM	Ig gamma-2b chain

RESULT 1

G2HU

Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

R;Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; P

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f

A;Reference number: A92809; MUID:81007873; PMID:6774012

A;Contents: myeloma protein Til

A;Accession: A92809

A;Molecule type: protein

A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>

A;Note: Trp-156 is at or near the complement-binding site

R;Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of a

A;Reference number: A90752; MUID:80001357; PMID:113060

A;Contents: myeloma protein Zie

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-

A;Note: this sequence has since been revised

R;Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A;Reference number: A93132; MUID:80114419; PMID:118920

A;Contents: Zie

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <HOF>

R;Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A;Reference number: A94591

A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati

ned

R;Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Reference number: A90253; MUID:72033500; PMID:4940472

A;Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124; PMID:5782707  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGH2  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 14q32.33-14q32.33  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;133-202/Domain: immunoglobulin homology <IM2>  
F;239-306/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83,140-200,246-304/Disulfide bonds: #status experimental  
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.48; Score 554; DB 1; Length 326;  
Best Local Similarity 93.68; Pred. No. 3.2e-47;  
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
DB 111 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170

QY 61 REQSYNSTYRVSVLTTLVHQLDNLGKEYCKCKVSNKGLPSSIEKTIKAK 109  
DB 171 REQSYNSTYRVSVLTTLVHQLDNLGKEYCKCKVSNKGLPAPIETKISKAK 219

RESULT 2  
PT0207  
Ig gamma chain C region - chimpanzee  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C;Accession: PT0207  
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A;Reference number: PT0207; MUID:91287716; PMID:2062315  
A;Accession: PT0207  
A;Molecule type: mRNA  
A;Residues: 1-234 <EHR>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;48-117/Domain: immunoglobulin homology <IMW>

Query Match 93.8%; Score 545; DB 2; Length 234;  
Best Local Similarity 91.2%; Pred. No. 1.7e-46;  
Matches 104; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 55  
DB 21 PPVAPELLGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 80

QY 56 AKTKPREQVNSTYRVSVLTTLVHQLDNLGKEYCKCKVSNKGLPSSIEKTIKAK 109  
DB 81 AKTKPREQVNSTYRVSVLTTLVHQLDNLGKEYCKCKVSNKGLPAPIETKISKAK 134

RESULT 3  
S31866  
Ig gamma-1 chain C region - synthetic  
C;Species: synthetic  
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C;Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C;Accession: S31866  
R;Filipula, D.  
submitted to the EMBL Data Library, February 1993

A;Description: Screening method for protein-protein interactions of cloned gene products.  
A;Reference number: S31866  
A;Accession: S31866  
A;Molecule type: mRNA  
A;Residues: 1-255 <FIL>  
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
C;Keywords: immunoglobulin  
F;1-22/Region: Escherichia coli outer membrane protein A precursor  
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 93.5%; Score 543; DB 4; Length 255;  
Best Local Similarity 90.4%; Pred. No. 3e-46;  
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 55  
DB 35 PPVAPPELLGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 94

QY 56 AKTKPREQVNSTYRVSVLTTLVHQLDNLGKEYCKCKVSNKGLPSSIEKTIKAK 109  
DB 95 AKTKPREQVNSTYRVSVLTTLVHQLDNLGKEYCKCKVSNKGLPAPIETKISKAK 148

RESULT 4  
GHU  
Ig gamma-1 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A;Reference number: A93433; MUID:82274238; PMID:6287432  
A;Accession: A93433  
A;Molecule type: DNA  
A;Residues: 1-330 <ELL>  
A;Cross-references: UNIPROT:P01857; EMBL:Z17370  
A;Note: this sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) markers; R;Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S33904  
A;Accession: S36861  
A;Molecule type: DNA  
A;Residues: 2-330 <HAR>  
A;Cross-references: EMBL:Z17370  
R;Takahashi, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A;Reference number: S33887; MUID:83001943; PMID:6811139  
A;Accession: S33887  
A;Molecule type: DNA  
A;Residues: 88-113;235-330 <TAK>  
A;Cross-references: EMBL:Z17370  
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.  
Biochemistry 9, 3161-3170, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequence  
A;Reference number: A90563; MUID:71064024; PMID:5489771  
A;Accession: B90563  
A;Contents: myeloma protein Eu  
A;Molecule type: protein  
A;Residues: 1-96, 'R', 98-135 <CUN>  
A;Note: this sequence has the Gln(3) marker, 97-Arg  
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence  
A;Reference number: A90564; MUID:71064025; PMID:5530842  
A;Accession: A90564  
A;Molecule type: protein  
A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'R', 241-Met  
R;Ponstingl, H.; Hilschmann, N.



Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), Igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269; PMID:826475

A:Contents: myeloma protein Nie

A:Accession: B91668

A:Molecule type: protein

A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 277-300, 'E', 302-316, 'D', 318-330, 'E', 332-346, 'D', 348-362, 'E', 364-378, 'D', 380-394, 'E', 396-410, 'D', 412-426, 'E', 428-442, 'D', 444-458, 'E', 460-474, 'D', 476-490, 'E', 492-506, 'D', 508-522, 'E', 524-538, 'D', 540-554, 'E', 556-570, 'D', 572-586, 'E', 588-602, 'D', 604-618, 'E', 620-634, 'D', 636-650, 'E', 652-666, 'D', 668-682, 'E', 684-698, 'D', 700-714, 'E', 716-730, 'D', 732-746, 'E', 748-762, 'D', 764-778, 'E', 780-794, 'D', 796-810, 'E', 812-826, 'D', 828-842, 'E', 844-858, 'D', 860-874, 'E', 876-890, 'D', 892-906, 'E', 908-922, 'D', 924-938, 'E', 940-954, 'D', 956-970, 'E', 972-986, 'D', 988-1002, 'E', 1004-1018, 'D', 1020-1034, 'E', 1036-1050, 'D', 1052-1066, 'E', 1068-1082, 'D', 1084-1098, 'E', 1100-1114, 'D', 1116-1130, 'E', 1132-1146, 'D', 1148-1162, 'E', 1164-1178, 'D', 1180-1194, 'E', 1196-1210, 'D', 1212-1226, 'E', 1228-1242, 'D', 1244-1258, 'E', 1260-1274, 'D', 1276-1290, 'E', 1292-1306, 'D', 1308-1322, 'E', 1324-1338, 'D', 1340-1354, 'E', 1356-1370, 'D', 1372-1386, 'E', 1388-1402, 'D', 1404-1418, 'E', 1420-1434, 'D', 1436-1450, 'E', 1452-1466, 'D', 1468-1482, 'E', 1484-1498, 'D', 1500-1514, 'E', 1516-1530, 'D', 1532-1546, 'E', 1548-1562, 'D', 1564-1578, 'E', 1580-1594, 'D', 1596-1610, 'E', 1612-1626, 'D', 1628-1642, 'E', 1644-1658, 'D', 1660-1674, 'E', 1676-1690, 'D', 1692-1706, 'E', 1708-1722, 'D', 1724-1738, 'E', 1740-1754, 'D', 1756-1770, 'E', 1772-1786, 'D', 1788-1802, 'E', 1804-1818, 'D', 1820-1834, 'E', 1836-1850, 'D', 1852-1866, 'E', 1868-1882, 'D', 1884-1898, 'E', 1900-1914, 'D', 1916-1930, 'E', 1932-1946, 'D', 1948-1962, 'E', 1964-1978, 'D', 1980-1994, 'E', 1996-2010, 'D', 2012-2026, 'E', 2028-2042, 'D', 2044-2058, 'E', 2060-2074, 'D', 2076-2090, 'E', 2092-2106, 'D', 2108-2122, 'E', 2124-2138, 'D', 2140-2154, 'E', 2156-2170, 'D', 2172-2186, 'E', 2188-2202, 'D', 2204-2218, 'E', 2220-2234, 'D', 2236-2250, 'E', 2252-2266, 'D', 2268-2282, 'E', 2284-2298, 'D', 2300-2314, 'E', 2316-2330, 'D', 2332-2346, 'E', 2348-2362, 'D', 2364-2378, 'E', 2380-2394, 'D', 2396-2410, 'E', 2412-2426, 'D', 2428-2442, 'E', 2444-2458, 'D', 2460-2474, 'E', 2476-2490, 'D', 2492-2506, 'E', 2508-2522, 'D', 2524-2538, 'E', 2540-2554, 'D', 2556-2570, 'E', 2572-2586, 'D', 2588-2602, 'E', 2604-2618, 'D', 2620-2634, 'E', 2636-2650, 'D', 2652-2666, 'E', 2668-2682, 'D', 2684-2698, 'E', 2700-2714, 'D', 2716-2730, 'E', 2732-2746, 'D', 2748-2762, 'E', 2764-2778, 'D', 2780-2794, 'E', 2796-2810, 'D', 2812-2826, 'E', 2828-2842, 'D', 2844-2858, 'E', 2860-2874, 'D', 2876-2890, 'E', 2892-2906, 'D', 2908-2922, 'E', 2924-2938, 'D', 2940-2954, 'E', 2956-2970, 'D', 2972-2986, 'E', 2988-3002, 'D', 3004-3018, 'E', 3020-3034, 'D', 3036-3050, 'E', 3052-3066, 'D', 3068-3082, 'E', 3084-3098, 'D', 3100-3114, 'E', 3116-3130, 'D', 3132-3146, 'E', 3148-3162, 'D', 3164-3178, 'E', 3180-3194, 'D', 3196-3210, 'E', 3212-3226, 'D', 3228-3242, 'E', 3244-3258, 'D', 3260-3274, 'E', 3276-3290, 'D', 3292-3306, 'E', 3308-3322, 'D', 3324-3338, 'E', 3340-3354, 'D', 3356-3370, 'E', 3372-3386, 'D', 3388-3402, 'E', 3404-3418, 'D', 3420-3434, 'E', 3436-3450, 'D', 3452-3466, 'E', 3468-3482, 'D', 3484-3498, 'E', 3500-3514, 'D', 3516-3530, 'E', 3532-3546, 'D', 3548-3562, 'E', 3564-3578, 'D', 3580-3594, 'E', 3596-3610, 'D', 3612-3626, 'E', 3628-3642, 'D', 3644-3658, 'E', 3660-3674, 'D', 3676-3690, 'E', 3692-3706, 'D', 3708-3722, 'E', 3724-3738, 'D', 3740-3754, 'E', 3756-3770, 'D', 3772-3786, 'E', 3788-3802, 'D', 3804-3818, 'E', 3820-3834, 'D', 3836-3850, 'E', 3852-3866, 'D', 3868-3882, 'E', 3884-3898, 'D', 3900-3914, 'E', 3916-3930, 'D', 3932-3946, 'E', 3948-3962, 'D', 3964-3978, 'E', 3980-3994, 'D', 3996-4010, 'E', 4012-4026, 'D', 4028-4042, 'E', 4044-4058, 'D', 4060-4074, 'E', 4076-4090, 'D', 4092-4106, 'E', 4108-4122, 'D', 4124-4138, 'E', 4140-4154, 'D', 4156-4170, 'E', 4172-4186, 'D', 4188-4202, 'E', 4204-4218, 'D', 4220-4234, 'E', 4236-4250, 'D', 4252-4266, 'E', 4268-4282, 'D', 4284-4298, 'E', 4300-4314, 'D', 4316-4330, 'E', 4332-4346, 'D', 4348-4362, 'E', 4364-4378, 'D', 4380-4394, 'E', 4396-4410, 'D', 4412-4426, 'E', 4428-4442, 'D', 4444-4458, 'E', 4460-4474, 'D', 4476-4490, 'E', 4492-4506, 'D', 4508-4522, 'E', 4524-4538, 'D', 4540-4554, 'E', 4556-4570, 'D', 4572-4586, 'E', 4588-4602, 'D', 4604-4618, 'E', 4620-4634, 'D', 4636-4650, 'E', 4652-4666, 'D', 4668-4682, 'E', 4684-4698, 'D', 4700-4714, 'E', 4716-4730, 'D', 4732-4746, 'E', 4748-4762, 'D', 4764-4778, 'E', 4780-4794, 'D', 4796



A;Accession: I47162  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A;Residues: 1-277 <KAC>  
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130  
C;Genetics:  
A;Gene: IGGA  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match      78.0%; Score 453; DB 2; Length 277;  
Best Local Similarity    77.9%; Pred.No. 2.6e-37;  
Matches         81; Conservative    14; Mismatches    9; Indels          0; Gaps           0;

Qy      6 GPSVLFPPPKDMLMSRTPETCVVDVSHSDPEVKFNWYDVGVHNAKTKPREEQY 65  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      65 GPFAIFFPKKDTLMISRTPKVTCTVVDDVSQNENPFQSWSYVDGVEVHTAQTRPKEGF 124

Qy      66 NSTYRVSVSLTVLDHWLNCKEYKCYSNKGLPSSIEKTTISKAK 109  
     ||||| : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      125 NSTYRVSVLP IQHDWLNGKFCKCNKNKDLPAPITRIISKAK 168

RESULT 13  
I47161  
Ig gamma 3 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47161  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s...  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
A;Accession: I47161  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128  
C;Genetics:  
A;Gene: IGGB  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F:I33-202/Domain: immunoglobulin homology <IMM>

Query Match      76.1%; Score 442; DB 2; Length 328;  
Best Local Similarity    77.1%; Pred.No. 3.9e-36;  
Matches         81; Conservative    13; Mismatches   11; Indels          0; Gaps           0;

Qy      4 VAGPSVFLLPPPKDQLMISRTEPTVCVVVDVSHDEDPKPNWYDVGVHNATKYPREE 63  
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      114 VAGPSVFIPPPPKDQLMISQTPEVTCVVVDVSKHAEOFSWYVDGVEVHTAEIRPKEE 173

Qy      64 QYNSTYRVSVSLTVLDHWLNCKEYKCYSNKGLPSSIETTKISA 108  
     ||||| : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      174 QNSTYRVSVSFLPIQHODWLKGFKFCNVNNVDLPAPIITRKISA 218

RESULT 14  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Sep-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47158  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s...  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
A;Accession: I47158  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122  
C;Genetics:  
A;Gene: IGGI



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 79.8836 Seconds  
(without alignments)  
698.725 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVLFPPKPKDIL.....CKVSNKGLPSSIEKTIKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	554	95.4	326	1	GC2_HUMAN	P01859 homo sapien
2	554	95.4	417	2	Q6N093	Q6n093 homo sapien
3	554	95.4	465	2	Q6P6C4	Q6p6c4 homo sapien
4	551	94.8	464	2	Q6MZU6	Q6mzu6 homo sapien
5	545	93.8	493	2	Q68CN4	Q68cn4 homo sapien
6	543	93.5	330	1	GC1_HUMAN	P01857 homo sapien
7	543	93.5	348	2	Q6PTX1	Q6pty1 homo sapien
8	543	93.5	465	2	Q6GMX6	Q6gmxx6 homo sapien
9	543	93.5	466	2	Q6IN78	Q6in78 homo sapien
10	543	93.5	469	2	Q727P5	Q7z7p5 homo sapien
11	543	93.5	470	2	Q6PJA4	Q6pja4 homo sapien
12	543	93.5	470	2	Q725W1	Q7z5w1 homo sapien
13	543	93.5	472	2	Q6N089	Q6n089 homo sapien
14	543	93.5	473	2	Q6MZV7	Q6mzv7 homo sapien
15	543	93.5	473	2	Q6P055	Q6p055 homo sapien
16	543	93.5	475	2	Q6GMW7	Q6gmw7 homo sapien
17	543	93.5	475	2	Q6MZQ6	Q6mzq6 homo sapien
18	543	93.5	475	2	Q6N095	Q6n095 homo sapien
19	543	93.5	476	2	Q6GMX1	Q6gmxx1 homo sapien
20	543	93.5	478	2	Q6P181	Q6p181 homo sapien
21	543	93.5	480	2	Q6N094	Q6n094 homo sapien
22	543	93.5	480	2	Q6PJF1	Q6pjf1 homo sapien
23	543	93.5	481	2	Q6N097	Q6n097 homo sapien
24	543	93.5	482	2	Q72351	Q7z351 homo sapien
25	543	93.5	544	2	Q6P095	Q6p095 homo sapien
26	543	93.5	679	2	Q96PQ8	Q96pq8 homo sapien
27	540	92.9	327	1	GC4_HUMAN	P01861 homo sapien
28	540	92.9	466	2	Q6N096	Q6n096 homo sapien
29	540	92.9	473	2	Q8TC63	Q8tc63 homo sapien
30	538	92.6	487	2	Q652L2	Q652l2 mus sp. fv/
31	537	92.4	476	2	Q6MZX7	Q6mzx7 homo sapien

32	524	90.2	354	2	Q86TT2	Q86tt2 homo sapien
33	524	90.2	518	2	Q6N030	Q6n030 homo sapien
34	520	89.5	509	2	Q8NF17	Q8nf17 homo sapien
35	520	89.5	521	2	Q8N4Y9	Q8n4y9 homo sapien
36	504	86.7	290	1	GC3_HUMAN	P01860 homo sapien
37	443	76.2	337	2	Q95M34	Q95m34 equus caball
38	420	72.3	333	1	GC8_RAT	P20761 rattus norv
39	417	71.8	329	1	GC2_CAVPO	P01882 cavia porce
40	413	71.1	323	1	GC_FABIT	P01870 oryctolagus
41	410.5	70.7	303	2	Q6KAM2	Q6kam2 mus musculus
42	410.5	70.7	329	1	GC3_MOUSE	P22436 mus musculus
43	410.5	70.7	398	1	GC3M_MOUSE	P03987 mus musculus
44	410.5	70.7	470	2	Q7TMK1	Q7tmk1 mus musculus
45	396	68.2	324	1	GC1_MOUSE	P01868 mus musculus

#### ALIGNMENTS

RESULT 1  
GC2\_HUMAN  
ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 03-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig gamma-2 chain C region.  
GN Name=IGHG2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellison J W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy  
RT chain constant region genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;  
RA Takahashi N., Ueda S., Obata M., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for  
RT evolution of a gene family.";  
RL Cell 29:671-679(1982).  
RN [3]  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
RT genes.";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
RT evolutionary, and functional implications.";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=80001357; PubMed=113060;  
RA Connell G.E., Farr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
RT domains of a human IgG2 myeloma protein.";  
RL Can. J. Biochem. 57:758-767(1979).  
RN [6]  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;



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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Moore T., Max S.I., Wang J., Heide F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAG2335.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD89348AD37B6D CRC64;

Query Match 95.4%; Score 554; DB 2; Length 465;
Best Local Similarity 93.6%; Pred. No. 4.7e-46;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 250 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 309

Qy 61 REEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAK 109
Db 310 REEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIEKTISKTK 358

RESULT 4
Q6MZU6
ID Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAB45931.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 94.8%; Score 551; DB 2; Length 464;
Best Local Similarity 92.7%; Pred. No. 9.3e-46;
Matches 101; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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Db 249 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 308

Qy 61 REEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAK 109
Db 309 REEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIEKTISKTK 357

RESULT 5
Q68CN4
ID Q68CN4 PRELIMINARY; PRT; 493 AA.
AC Q68CN4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209 (Fragment).
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749861; CAH18705.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3F8AB40 CRC64;

Query Match 93.8%; Score 545; DB 2; Length 493;
```

Best Local Similarity 91.7%; Pred. No. 3.9e-45;  
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDITLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 278 APPVAGSAFLFPKPKDITLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 337  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 REEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTIKAK 109  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 338 REEQFNSTYRVSVLTVVHODWLNKKEYCKVSNKGLPAPIEXTISKTK 386  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

## RESULT 6

GC1\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino  
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic  
RT peptides of the H-chain, alignment of the tryptic peptides and  
RT discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary  
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;

RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein NIE). I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RL Biochemistry 20:2361-2370(1981).  
CC -!- MISCELLANEOUS: NIE has the G1M(17) allotypic marker, 97-K, and the  
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
CC G1M(3) marker and the G1M (non-1) markers.  
CC -!- MISCELLANEOUS: NIE also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J00228; AAC82527.1; ALT\_INIT.  
DR PIR: A93433; GHU.  
DR PDB: 1AU7; X-ray; H=1-103.  
DR PDB: 1DSB; X-ray; B/H=1-101.  
DR PDB: 1D51; X-ray; H=1-101.  
DR PDB: 1D6V; X-ray; H=1-101.  
DR PDB: 1DN2; X-ray; A/B=120-326.  
DR PDB: 1E4K; X-ray; A/B=106-329.  
DR PDB: 1FC1; X-ray; A/B=106-329.  
DR PDB: 1FC2; X-ray; D=106-329.  
DR PDB: 1FCC; X-ray; A=121-326.  
DR PDB: 1HZH; X-ray; H/K=1-330.  
DR PDB: 1I1S; X-ray; B/D=1-103.  
DR PDB: 1I1X; X-ray; A/B=107-330.  
DR PDB: 1L6X; X-ray; A=120-326.  
DR PDB: 1QOX; X-ray; A/B=119-330.  
DR PDB: 2RCS; X-ray; H=1-103.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM; 147100; -.  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; F:antigen binding; TAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00447; Ig; 3.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW 3D-structure; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 Hinge.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83  
FT DISULFID 103 103 Interchain (with light chain).  
FT DISULFID 109 109 Interchain (with heavy chain).  
FT DISULFID 112 112 Interchain (with heavy chain).  
FT DISULFID 144 204



## RESULT 7



DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051328; AAH51328.1; -.  
DR HSSP; P01857; 1H2H.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 93.5%; Score 543; DB 2; Length 470;  
Best Local Similarity 90.4%; Pred. No. 5.8e-45;  
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 55  
||| : |||||  
DB 249 PCPCPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHN 308  
||| : |||||  
QY 56 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTSKAK 109  
||| : |||||  
DB 309 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTSKAK 362  
||| : |||||

RESULT 11  
ID Q6PJA4 PRELIMINARY; PRT; 470 AA.  
AC Q6PJA4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAH53984.1; -.  
DR HSSP; P01857; 1H2H.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003599; Ig\_v.  
DR InterPro; IPR003596; Ig\_v.

RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051328; AAH51328.1; -.  
DR HSSP; P01857; 1H2H.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR003599; Ig\_v.

RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018747; AAH18747.1; -.  
DR HSSP; P01861; 1A0Q.  
DR InterPro; IPR003599; Ig\_v.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC051328; AAH51328.1; -.  
DR HSSP; P01857; 1HZH.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 93.5%; Score 543; DB 2; Length 470;  
Best Local Similarity 90.4%; Pred. No. 5.8e-45;  
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1

QY 2 PP-----VAGPSVFPPPKKDTLMISRTPEVTCCVVVDVSHEDDEVKFNMYVDGVEVHN 55  
||| : |||||  
DB 249 PCPCPELLGGSPVFLFPFKPKDTLMISRTPEVTCCVVVDVSHEDDEVKFNMYVDGVEVHN 308  
||| : |||||  
QY 56 AKTKPREEQNSTYRVSVLTVLHQDLNGKEYCKVSKNGLPSSIETISKAK 109  
||||| : |||||  
DB 309 AKTKPREEQNSTYRVSVLTVLHQDLNGKEYCKVSKNGLPSSIETISKAK 362  
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RESULT 11  
ID Q6PJ4 PRELIMINARY; PRT; 470 AA.  
AC Q6PJ4  
CD Q6PJ4  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Udwin T.B., Toshuyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.E.,  
RA Brownstein M.J., Soares M.B., Donald M.P., Casavant T.E., Mullahy S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Krzywinski M.I., Skalska U., Smutsky J., Myers R.M., Butterfield Y.S.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC053984; AAH53984.1; -.  
DR HSSP; P01857; 1HZH.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003599; IG\_V.

RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC018747; AAH18747.1; -.  
DR HSSP; P01861; 1ADO.  
DR InterPro; IPR003599; IG\_V.

```
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match          93.5%; Score 543; DB 2; Length 470;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
   ||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 250 PCPAPPELLGGPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 309
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

QY 56 AKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 109
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 310 AKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPAPIEKTIISKAK 363
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 13
Q6N089
ID Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFp686P15220.
GN Names=DKFp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match          93.5%; Score 543; DB 2; Length 472;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
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Db 252 PCPAPPELLGGPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 311
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QY 56 AKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 109
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 312 AKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPAPIEKTIISKAK 365
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 14
Q6MZV7
ID Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFp686C11235.
GN Names=DKFp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAB4C0BFC447 CRC64;

Query Match          93.5%; Score 543; DB 2; Length 473;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
   ||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
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   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

QY 56 AKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 109
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 313 AKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPAPIEKTIISKAK 366
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 15
Q6P055
ID Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
```

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Peripheral Nervous System;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the ENBL/GenBank/DBBJ databases.  
DR EMBL; BC065820; AAH65820.1; -;  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF07654; C1-Bet; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 93.5%; Score 543; DB 2; Length 473;  
Best Local Similarity 90.4%; Pred. No. 5.8e-45;  
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy	2	PP-----VAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
Db	253	PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 312
Qy	56	AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db	313	AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 366

Search-completed: November 17, 2005, 07:10:19  
Job time : 81.8836 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 06:51:22 ; Search time 24.3881 Seconds  
(without alignments)  
333.636 Million cell updates/sec

Title: US-09-674-857-1  
Perfect score: 581  
Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTIISKAK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	96.2	448	4	US-09-968-362A-18
2	554	95.4	109	3	US-08-444-644-30
3	554	95.4	109	3	US-08-232-246A-30
4	554	95.4	217	4	US-09-483-588-5
5	554	95.4	228	4	US-09-968-362A-27
6	554	95.4	432	3	US-08-477-460B-2
7	554	95.4	432	3	US-08-379-516-2
8	554	95.4	432	3	US-09-329-916-2
9	554	95.4	432	3	US-08-485-372A-2
10	554	95.4	432	3	US-09-409-006A-2
11	554	95.4	432	4	US-08-484-681-1
12	554	95.4	432	4	US-09-766-995-2
13	554	95.4	432	5	PCT-US93-07422-2
14	554	95.4	451	4	US-09-472-087-70
15	554	95.4	463	4	US-09-472-087-1
16	554	95.4	463	4	US-09-472-087-4
17	554	95.4	463	4	US-09-472-087-63
18	554	95.4	463	4	US-09-472-087-68
19	554	95.4	464	4	US-09-472-087-2
20	554	95.4	464	4	US-09-472-087-66
21	554	95.4	470	4	US-09-859-053-28
22	554	95.4	470	4	US-09-859-053-32
23	554	95.4	470	4	US-09-859-053-36
24	554	95.4	530	3	US-08-477-460B-4
25	554	95.4	530	3	US-08-379-516-4
26	554	95.4	530	3	US-09-329-916-4
27	554	95.4	530	3	US-08-485-372A-4

28	554	95.4	530	3	US-09-409-006A-4	Sequence 4, Appli
29	554	95.4	530	4	US-08-484-681-4	Sequence 4, Appli
30	554	95.4	530	4	US-09-766-995-4	Sequence 4, Appli
31	554	95.4	530	5	PCT-US93-07422-4	Sequence 4, Appli
32	553	95.3	447	4	US-09-968-362A-22	Sequence 22, Appli
33	551	94.8	450	2	US-08-788-800-12	Sequence 12, Appli
34	551	94.8	469	2	US-07-934-373C-23	Sequence 23, Appli
35	551	94.8	469	3	US-08-437-642B-23	Sequence 23, Appli
36	551	94.8	469	4	US-08-146-206C-23	Sequence 23, Appli
37	551	94.8	469	4	US-09-705-686-23	Sequence 23, Appli
38	551	94.8	469	4	US-09-705-392A-23	Sequence 23, Appli
39	551	94.8	469	4	US-09-705-398-23	Sequence 23, Appli
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41	548	94.3	463	4	US-09-472-087-64	Sequence 64, Appli
42	548	94.3	468	3	US-09-485-737B-67	Sequence 67, Appli
43	548	94.3	468	4	US-10-071-485-67	Sequence 90, Appli
44	548	94.3	711	3	US-09-485-737B-90	Sequence 90, Appli
45	548	94.3	711	4	US-10-071-485-90	Sequence 90, Appli

ALIGNMENTS

RESULT 1  
US-09-968-362A-18  
; Sequence 18, Application US/09968362A  
; Patent No. 6797493  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUN2001  
; CURRENT APPLICATION NUMBER: US/09/968,362A  
; CURRENT FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 18  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hG-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure 1)  
; OTHER INFORMATION: 2A)  
US-09-968-362A-18

Query Match	96.2%	Score	559	DB	4	Length	448
Best Local Similarity	94.5%	Pred. No.	4e-56				
Matches	103	Conservative	5	Mismatches	1	Indels	0
Gaps	0						
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DB	233	APPVAGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP	292				
QY	61	REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	109				
DB	293	REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	341				

RESULT 2  
US-08-444-644-30  
; Sequence 30, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive

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; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1989
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match 95.4%; Score 554; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKTK 109

RESULT 3
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6323508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match 95.4%; Score 554; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.4e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKTK 109

RESULT 4
US-09-483-588-5
; Sequence 5, Application US/09483588
; Patent No. 6737056
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; FILE REFERENCE: P1726R1
; CURRENT APPLICATION NUMBER: US/09/483,588
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: US 60/116,023
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-483-588-5

Query Match 95.4%; Score 554; DB 4; Length 217;
Best Local Similarity 93.6%; Pred. No. 5.9e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
QY 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
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ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/329,916  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,450  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-09-329-916-2

Query Match 95.4%; Score 554; DB 3; Length 432;  
Best Local Similarity 93.8%; Pred. No. 1.4e-55;  
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
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Db 277 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 9  
US-08-485-372A-2  
Sequence 2, Application US/08485372A  
Patent No. 6187748  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,372A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,227  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-II-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-485-372A-2

Query Match 95.4%; Score 554; DB 3; Length 432;  
Best Local Similarity 93.6%; Pred. No. 1.4e-55;  
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
Db 217 APPVAGPSVFLFPKPKDTLMISRTEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276

QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109  
Db 277 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 10  
US-09-409-006A-2  
Sequence 2, Application US/09409006A  
Patent No. 6342586  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/409,006A  
FILING DATE: 29-SEP-1999  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: homo sapien

CELL TYPE: lymphocyte

US-09-409-006A-2

Query Match 95.4%; Score 554; DB 3; Length 432;

Best Local Similarity 93.6%; Pred. No. 1.4e-55;

Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 276

Qy 61 REEQYNSTYRVSVLTIVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 109

Db 277 REEQFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIEKTISKTK 325

## RESULT 11

US-08-484-681-2

Sequence 2, Application US/08484681

Patent No. 6451313

GENERAL INFORMATION:

APPLICANT: Beaudry, Gary A.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,681

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 37690-II-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: homo sapien

CELL TYPE: lymphocyte

US-08-484-681-2

Query Match 95.4%; Score 554; DB 4; Length 432;

Best Local Similarity 93.6%; Pred. No. 1.4e-55;

Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 276

Qy 61 REEQYNSTYRVSVLTIVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 109

Db 277 REEQFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIEKTISKTK 325

## RESULT 12

US-09-766-995-2

Sequence 2, Application US/09766995

Patent No. 6737267

GENERAL INFORMATION:

APPLICANT: Graham P. Allaway et al.

TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF

FILE REFERENCE: 2048/41215-CB/JPW/SHS

CURRENT APPLICATION NUMBER: US/09/766,995

CURRENT FILING DATE: 2001-01-22

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 432

TYPE: PRT

ORGANISM: homo sapians

US-09-766-995-2

Query Match 95.4%; Score 554; DB 4; Length 432;

Best Local Similarity 93.6%; Pred. No. 1.4e-55;

Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 276

Qy 61 REEQYNSTYRVSVLTIVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAK 109

Db 277 REEQFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIEKTISKTK 325

## RESULT 13

PCT-US93-07422-2

Sequence 2, Application PC/TUS9307422

GENERAL INFORMATION:

APPLICANT: Progenics Pharmaceuticals, Inc.

TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07422

FILING DATE: 19930806

CLASSIFICATION:

PRIOR APPLICATION DATA: US 07/927,931

APPLICATION NUMBER: 07-AUG-1992

FILING DATE: 07-AUG-1992

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 977-9550
/ TELEFAX: (212) 977-9809
/ TELEX: 422523 COOP UI
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 432 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: homo sapien
/ CELL TYPE: lymphocyte
PCT-US93-07422-2

Query Match 95.4%; Score 554; DB 5; Length 432;
Best Local Similarity 93.6%; Pred. No. 1.4e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 217 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
Db 277 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325

RESULT 14
US-09-472-087-70
/ Sequence 70, Application US/09472087
/ Patent No. 6682736
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, ELLEN E.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1
/ CURRENT APPLICATION NUMBER: US/09/472,087
/ CURRENT FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 60/113,647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 70
/ LENGTH: 451
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-472-087-70

Query Match 95.4%; Score 554; DB 4; Length 451;
Best Local Similarity 93.6%; Pred. No. 1.5e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 236 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 295
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
Db 296 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 344
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RESULT 15

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US-09-472-087-1
/ Sequence 1, Application US/09472087
/ Patent No. 6682736
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, ELLEN E.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1
/ CURRENT APPLICATION NUMBER: US/09/472,087
/ CURRENT FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 60/113,647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 463
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-472-087-1

Query Match 95.4%; Score 554; DB 4; Length 463;
Best Local Similarity 93.6%; Pred. No. 1.6e-55;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 248 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 307
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
Db 308 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 356

Search completed: November 17, 2005, 07:13:20
Job time : 25.3881 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 07:05:08 ; Search time 83.6164 Seconds  
(without alignments)  
545.427 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APVAGPSVFLFPFKPXTL.....CKVSNKGLPSIEKTIKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	581	100.0	329	20	US-11-102-403-25
2	573	98.6	109	18	US-10-959-318-11
3	573	98.6	109	18	US-10-959-318-12
4	567	97.5	449	16	US-10-493-676-11
5	565	97.2	472	14	US-10-006-593-67
6	565	97.2	472	15	US-10-307-724-67
7	565	97.2	472	12	US-10-737-290-67
8	562.5	96.8	110	18	US-10-959-318-9
9	562.5	96.8	110	18	US-10-959-318-10
10	562	96.7	447	16	US-10-745-775-16
11	559	96.2	109	18	US-10-959-318-15

Query Match 100.0%; Score 581; DB 20; Length 329;  
Best Local Similarity 100.0%; Pred. No. 1.1e-48;

12	559	96.2	109	18	US-10-959-318-16	Sequence 16, Appl
13	559	96.2	436	10	US-09-932-812-18	Sequence 18, Appl
14	559	96.2	436	16	US-10-761-593A-18	Sequence 18, Appl
15	559	96.2	436	20	US-11-016-518A-18	Sequence 18, Appl
16	559	96.2	436	20	US-11-017-185-18	Sequence 18, Appl
17	559	96.2	448	10	US-09-968-362-18	Sequence 18, Appl
18	559	96.2	448	16	US-10-800-497-18	Sequence 18, Appl
19	559	96.2	448	16	US-10-800-449-18	Sequence 18, Appl
20	554	95.4	109	18	US-10-959-318-2	Sequence 2, Appl
21	554	95.4	217	9	US-09-813-341-3	Sequence 3, Appl
22	554	95.4	217	14	US-10-277-370-3	Sequence 3, Appl
23	554	95.4	217	14	US-10-196-394-74	Sequence 74, Appl
24	554	95.4	217	15	US-10-370-749-16	Sequence 16, Appl
25	554	95.4	217	16	US-10-835-642-5	Sequence 5, Appl
26	554	95.4	217	16	US-10-757-863-5	Sequence 5, Appl
27	554	95.4	217	17	US-10-982-470-5	Sequence 5, Appl
28	554	95.4	217	20	US-11-158-839-5	Sequence 3, Appl
29	554	95.4	228	15	US-10-466-593-3	Sequence 3, Appl
30	554	95.4	228	16	US-10-761-593A-27	Sequence 27, Appl
31	554	95.4	228	16	US-10-800-497-27	Sequence 27, Appl
32	554	95.4	228	16	US-10-800-449-27	Sequence 27, Appl
33	554	95.4	228	20	US-11-016-518A-27	Sequence 27, Appl
34	554	95.4	228	20	US-11-017-185-27	Sequence 27, Appl
35	554	95.4	310	16	US-10-684-109-75	Sequence 75, Appl
36	554	95.4	326	13	US-10-047-542-22	Sequence 22, Appl
37	554	95.4	326	14	US-10-310-719-9	Sequence 9, Appl
38	554	95.4	326	14	US-10-112-582-2	Sequence 2, Appl
39	554	95.4	326	15	US-10-038-591-28	Sequence 28, Appl
40	554	95.4	326	15	US-10-656-769-6	Sequence 6, Appl
41	554	95.4	326	16	US-10-775-444A-28	Sequence 28, Appl
42	554	95.4	326	16	US-10-756-153-32	Sequence 32, Appl
43	554	95.4	326	17	US-10-872-932A-37	Sequence 37, Appl
44	554	95.4	326	17	US-10-928-305-8	Sequence 8, Appl
45	554	95.4	326	17	US-10-891-658-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-11-102-403-25  
; Sequence 25, Application US/11102403  
; Publication No. US20050226876A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAUS, YVO  
; APPLICANT: HIMBER, JACQUES  
; APPLICANT: JANSEN-MOLENAAR, MIRANDA  
; APPLICANT: KLING, DOROTHEE  
; APPLICANT: KOPETZKI, ERHARD  
; APPLICANT: PARRIN, PAUL  
; APPLICANT: REBERS, FRANK  
; APPLICANT: STEINER, BEAT  
; APPLICANT: STERN, ANNE  
; APPLICANT: STREIN, PAMELA  
; APPLICANT: STUBENRAUCH, KAY-GUNNAR  
; APPLICANT: VAN DE WINKEL, JAN  
; APPLICANT: VAN VUGT, MARTINE  
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES  
; FILE REFERENCE: 22354  
; CURRENT APPLICATION NUMBER: US/11/102,403  
; PRIOR FILING DATE: 2005-04-08  
; PRIOR APPLICATION NUMBER: EP 04008722.3  
; PRIOR FILING DATE: 2004-04-13  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 25  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-102-403-25

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	APPVAGPSVFLPEPKDITLMI	SRPEVTCVVVDVSHEDPEVKFKNWYVDGVEVHNATKTP	60
Db	114	APPVAGPSVFLPEPKDITLMI	SRPEVTCVVVDVSHEDPEVKFKNWYVDGVEVHNATKTP	171
Qy	61	REQYNSTYRVYSVLT	VLVHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK	109
Db	174	REQYNSTYRVYSVLT	VLVHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK	222

## RESULT 2

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US-10-959-318-11
; Sequence 11, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-11

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Query Match      98.6%; Score 573; DB 18; Length 109;
Best Local Similarity 99.1%; Pred. No. 1.9e-48;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 APPVAGPSVFLPPPKDLMISRPEVTCCVVVDVSHEDPVEKFNWYDGVGEVHNATKP 60
|||||
Db 1 APPVAGPSVFLPPPKDLMISRPEVTCCVVVDVSOEDPVEKFNWYDGVGEVHNATKP 60
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### RESULT 3

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US-10-959-318-12
; Sequence 12, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and e (E268)

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US-10-959-318-12  
OTHER INFORMATION: mutations

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Query Match      98.6%; Score 573; DB 18; Length 109;
Best Local Similarity 99.1%; Pred. No. 1.9e-48;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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## RESULT 4

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US-10-493-676-11
; Sequence 11, Application US/10493676
; Publication No. US20040265306A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Arthos, James
; APPLICANT: Cicala, Claudia
; APPLICANT: Fauci, Anthony S.
; TITLE OF INVENTION: IMMUNOCONJUGATES COMPRISING CD4 AND IMMUNOGLOBULIN MOLECULES FOR
; TITLE OF INVENTION: THE TREATMENT OF HIV INFECTION
; FILE REFERENCE: 4239-68221
; CURRENT APPLICATION NUMBER: US/10/493,676
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: PCT/US02/34393
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/346,231
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FD1D2-Igatp
US-10-493-676-11

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Query Match	97.6%	Score 567;	DB 16;	Length 449;
Best Local Similarity	97.2%;	Pred. No. 3.6e-47;		
Matches 106;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy 1	APVAGPSVFLPPKPKDTLMI	SRTPEVTCVVVDVSHEDPEVF	KNWVVDGVEVHNATKP	60
Db 216	APVAGPSVFLPPKPKDTLMI	SRTPEVTCVVVDVSHEDPEVF	KNWVVDGVEVHNATKP	275
Qy 61	RSQYNSTVRVSVLTVLHODW	LNGKEYKCKVSNKGLPSSIE	KTISAK	109
Db 276	RSQYNSTVRVSVLTVLHODW	LNGKEYKCKVSNKGLPSSIE	KTISAK	324

RESULT 5

US-10-006-593-67  
; Sequence 67, Application US/10006593  
; Publication No. US20030049683A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
; FILE REFERENCE: 1087-2  
; CURRENT APPLICATION NUMBER: US/10/006,593  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/251,448  
; PRIOR FILING DATE: 2000-12-05

	Query Match	97.6%; Score 567; DB 16; Length 449;
	Best Local Similarity	97.2%; Pred. No. 3.6e-47;
	Matches	106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy	1	APPVAGPSVFLPPKPKDTLMI SRTPEVT CVVVDSHEDPEVFKNWYVDGVEVHNATKP 60       
Db	216	APPVAGPSVFLPPKPKDTLMI SRTPEVT CVVVDSHEDPEVFKNWYVDGVEVHNATKP 275       
Qy	61	RSQYNSTRVSVSLTVLHODWLNGEYKCKVSNKGILPSSIEKTISAK 109     :
Db	276	RSQYNSTRVSVSLTVLHODWLNGEYKCKVSNKALPAPIETISAK 324     :

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; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67

Query Match          97.2%; Score 565; DB 14; Length 472;
Best Local Similarity 97.2%; Pred. No. 6.1e-47;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 257 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316

QY 61 REEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 109
Db 317 REEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 365

RESULT 6
US-10-307-724-67
; Sequence 67, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67

Query Match          97.2%; Score 565; DB 15; Length 472;
Best Local Similarity 97.2%; Pred. No. 6.1e-47;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 257 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316

QY 61 REEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 109
Db 317 REEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 365

RESULT 7
US-10-737-290-67
; Sequence 67, Application US/10737290

```

```

; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orecchia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10/737,290
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-737-290-67

Query Match          97.2%; Score 565; DB 16; Length 472;
Best Local Similarity 97.2%; Pred. No. 6.1e-47;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 257 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316

QY 61 REEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 109
Db 317 REEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 365

RESULT 8
US-10-959-318-9
; Sequence 9, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L.
; APPLICANT: Clark, Michael R.
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-9

Query Match          96.8%; Score 562.5; DB 18; Length 110;
Best Local Similarity 98.2%; Pred. No. 2e-47;

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; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and e (E268)  
; OTHER INFORMATION: mutations  
US-10-959-318-16

Query Match 96.2%; Score 559; DB 18; Length 109;  
Best Local Similarity 96.3%; Pred. No. 4.4e-47;  
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
Db 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP 60  
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109  
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 109

RESULT 13  
US-09-932-812-18  
; Sequence 18, Application US/09932812  
; Publication No. US20030082749A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity  
; FILE REFERENCE: 02SUN2001  
; CURRENT APPLICATION NUMBER: US/09/932.812  
; CURRENT FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: A)  
US-09-932-812-18

Query Match 96.2%; Score 559; DB 10; Length 436;  
Best Local Similarity 94.5%; Pred. No. 2.1e-46;  
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
Db 221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 280  
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109  
Db 281 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTIISKTK 329

RESULT 14  
US-10-761-593A-18  
; Sequence 18, Application US/10761593A  
; Publication No. US20040175824A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological activity  
; FILE REFERENCE: 02SUN2001-A  
; CURRENT APPLICATION NUMBER: US/10/761,593A  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: 09/932812

; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: 2A)  
US-10-761-593A-18

Query Match 96.2%; Score 559; DB 16; Length 436;  
Best Local Similarity 94.5%; Pred. No. 2.1e-46;  
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
Db 221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 280  
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109  
Db 281 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTIISKTK 329

RESULT 15  
US-11-016-518A-18  
; Sequence 18, Application US/11016518A  
; Publication No. US20050124045A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity  
; FILE REFERENCE: 02SUN2004D1  
; CURRENT APPLICATION NUMBER: US/11/016,518A  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US 09/932,812  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: 2A)  
US-11-016-518A-18

Query Match 96.2%; Score 559; DB 20; Length 436;  
Best Local Similarity 94.5%; Pred. No. 2.1e-46;  
Matches 103; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
Db 221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 280  
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109  
Db 281 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTIISKTK 329

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Job time : 84.6164 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.0913 Seconds  
(without alignments)  
473.187 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVLFPPKPKDYL.....CKVSNKGLPSSIEKTSKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0  
Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1980s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	109	3	AAY54996 Mutated C
2	559.5	96.3	110	3	AAY54998 Mutated C
3	554	95.4	109	2	AAR41709 Undefined
4	554	95.4	109	3	AAY54997 Mutated C
5	542	93.3	109	7	Add25659 Binding d
6	542	93.3	110	2	AAR27680 Human imm
7	542	93.3	110	2	AAR41684 Undefined
8	542	93.3	110	8	Adh75385 Human IGG
9	541	93.1	105	2	AAY42626 Human IGG
10	540	92.9	109	2	AAR67438
11	540	92.9	110	2	AAR41717 Undefined
12	537	92.4	109	5	AAE28089
13	537	92.4	110	8	ADH75415 CH2 regio
14	536	92.3	110	8	ADL90103 Human imm
15	535	92.1	110	8	ADH75413 CH2 regio
16	534	91.9	109	7	Add25761 Binding d
17	528	90.9	102	8	ADJ52129 CH1 delet
18	526	90.5	102	8	ADJ52132 CH1 delet
19	518	89.2	110	2	AAR41713 Undefined
20	408	70.2	110	2	AAW71023 Mus muscu
21	382	65.7	110	1	AAP83207 Sequence
22	344	59.2	72	8	ADL15711 Human imm
23	329	56.6	66	2	AAR75349 C-gamma-1
24	329	56.6	66	2	AAR75351 C-gamma-1
25	305	52.5	76	8	ADL15713 Human imm

26	270	46.5	56	1	AAP83205 Sequence
27	269.5	46.4	56	1	AAP83204 Sequence
28	266	45.8	56	1	AAP83201 Sequence
29	266	45.8	56	1	AAP83202 Sequence
30	265.5	45.7	56	1	AAP83203 Sequence
31	264.5	45.5	56	1	AAP83206 Sequence
32	249	42.9	46	8	ADR59138 Human IGG
33	234	40.3	46	8	ADR59139 Human IGG
34	232.5	40.0	110	2	AAR33315 Variant I
35	221	38.0	46	8	ADR59142 Rhesus mo
36	215	37.0	46	8	ADR59143 Rhesus mo
37	209	36.0	46	8	ADR59140 Rhesus mo
38	203.5	35.0	46	8	ADR59141 Crab-eati
39	201.5	34.7	110	2	AAR33314 Variant I
40	199	34.3	96	3	AAB53640 Human col
41	198	34.1	46	8	ADR59148 Camel IGG
42	194	33.4	46	8	ADR59145 Pig IGG2a
43	193.5	33.3	110	2	AAR33693 Variant I
44	192	33.0	46	8	ADR59147 Llama IGG
45					

#### ALIGNMENTS

RESULT 1

AAV54996

ID AAY54996 standard; protein; 109 AA.

AC AAY54996;

XX

DT 17-FEB-2000 (first entry)

XX

DE Mutated CH2 sequence G1deltaaab.

XX

KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IGG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion.

OS Synthetic.

XX

PN WO9558572-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001441.

XX

PR 08-MAY-1998; 98GB-00009951.

XX

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX

PI Armour KL, Clark MR, Williamson LM;

XX

DR WPI; 2000-039075/03.

XX

PT Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

PT

XX Claim 12; Fig 17; 81pp; English.

PS

XX This sequence represents the mutated CH2 molecule G1deltaaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
CC molecule is used to bind a target molecule (especially FcgammaRIIb  
CC causing inhibition of B cell activation, mast cell degranulation or  
CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
CC binding of a second binding molecule, e.g. an antibody, to the target  
CC molecule. The binding molecule is useful for the treatment of graft-vs-  
CC host disease, organ transplant rejection, bone-marrow transplant  
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.  
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
CC coronary artery occlusion). The binding molecules do not activate  
CC complement or trigger cytotoxic activities through FcgammaR and desirable  
CC IgG properties have been retained. The polypeptides do not contain non-  
CC human amino acids, and are therefore likely to have reduced  
CC immunogenicity. Further, they still bind Protein A, which is consistent  
CC with being able to cross the human placenta through interaction with FcRn  
CC (neonatal Fc receptor)  
XX Sequence 109 AA;  
SQ  
  
Query Match 100.0%; Score 581; DB 3; Length 109;  
Best Local Similarity 100.0%; Pred. No. 7.5e-52;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 60  
DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 60  
  
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109  
DB 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109  
  
RESULT 2  
AAY54998  
ID AAY54998 standard; protein; 110 AA.  
XX  
AC AAY54998;  
XX  
DT 17-FEB-2000 (first entry)  
DE  
DE Mutated CH2 sequence G1deltaaac.  
XX  
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;  
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
KW bone-marrow transplant rejection; autoimmunity disease; asthma; allergy;  
KW alloimmune disorder; autoimmunity haemolytic anaemia; inflammatory disease;  
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
KW sickle cell anaemia; coronary artery occlusion.  
XX  
OS Synthetic.  
XX  
XX WO9558572-A1.  
PN  
XX  
XX 18-NOV-1999.  
PD  
XX  
PF 07-MAY-1999; 99WO-GB001441.  
PP  
XX  
PR 08-MAY-1998; 98GB-00009951.  
PR  
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
PA  
XX  
PI Armour KL, Clark MR, Williams LM;  
XX  
DR WPI; 2000-039075/03.  
XX  
XX Immunoglobulin-derived binding molecules that do not activate complement  
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin

PT properties.  
XX  
XX Claim 12, Fig 17; 81pp; English.  
XX  
CC This sequence represents the mutated CH2 molecule G1deltaaac, and is a  
CC binding molecule of the invention. The recombinant binding molecule is  
CC capable of binding a target molecule without triggering complement  
CC dependent lysis, or the cell-mediated destruction of the target  
CC host disease, organ transplant rejection, bone-marrow transplant  
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.  
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
CC coronary artery occlusion). The binding molecules do not activate  
CC complement or trigger cytotoxic activities through FcgammaR and desirable  
CC IgG properties have been retained. The polypeptides do not contain non-  
CC human amino acids, and are therefore likely to have reduced  
CC immunogenicity. Further, they still bind Protein A, which is consistent  
CC with being able to cross the human placenta through interaction with FcRn  
CC (neonatal Fc receptor)  
XX  
SQ Sequence 110 AA;  
  
Query Match 96.3%; Score 559.5; DB 3; Length 110;  
Best Local Similarity 98.2%; Pred. No. 1.2e-49;  
Matches 108; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 APPVA-GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59  
DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
  
QY 60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109  
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
  
RESULT 3  
AAR41709  
ID AAR41709 standard; protein; 109 AA.  
XX  
AC AAR41709;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-OCT-1993 (first entry)  
XX  
XX Undefined ORF2 encoded by plasmid pAH4625.  
XX  
XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;  
KW light; chain; variable; constant; region; anti-human; pAH4807;  
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;  
KW endothelial cell; conjugate; neuropharmacological; gamma-3; gamma-4;  
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;  
KW Parkinsons disease; Alzheimers disease; Sp2/0 cell.  
XX  
OS Synthetic.  
XX  
XX WO9310819-A1.  
PN  
XX  
XX 10-JUN-1993.  
PD  
XX  
XX 24-NOV-1992; 92WO-US010206.  
PF  
XX  
XX 26-NOV-1991; 91US-00800458.  
PR  
XX



XX US2003118592-A1.  
XX 26-JUN-2003.  
XX 25-JUL-2002; 2002US-00207655.  
XX 17-JAN-2001; 2001US-0367358P.  
XX 17-JAN-2002; 2002US-00053530.  
XX 03-JUN-2002; 2002US-0385691P.  
XX (GENE-) GENE-CRAFT INC.  
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
XX WPI; 2003-801317/75.  
XX New binding domain-immunoglobulin fusion protein, useful for treating a  
XX subject having or suspected of having a malignant condition or a B-cell  
XX disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
XX Disclosure; SEQ ID NO 220; 157pp; English.  
XX The invention relates to a binding domain-immunoglobulin fusion protein  
XX comprising a binding domain polypeptide that is fused to an  
XX immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
XX CH2 constant region polypeptide that is fused to the hinge region  
XX polypeptide, and an immunoglobulin heavy chain CH3 constant region  
XX polypeptide that is fused to the CH2 constant region polypeptide. The  
XX hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
XX hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
XX region polypeptide, derived from (a) having 3 or more cysteine residues;  
XX where the mutated human IgG1 immunoglobulin hinge region polypeptide  
XX contains 2 cysteine residues, where the first cysteine is not mutated; a  
XX mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
XX (a) having 3 or more cysteine residues, where the mutated human IgG1  
XX immunoglobulin hinge region polypeptide contains no more than one  
XX cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
XX polypeptide, derived from (a) having 3 or more cysteine residues; where  
XX the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
XX no cysteine residues. The binding domain-immunoglobulin fusion protein is  
XX capable of at least one immunological activity comprising antibody  
XX dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
XX binding domain polypeptide is capable of specifically binding to an  
XX antigen. Also included are an isolated polynucleotide encoding the  
XX binding domain-immunoglobulin fusion protein, a recombinant expression  
XX construct comprising the polynucleotide (operably linked to a promoter),  
XX a host cell transformed or transfected with a recombinant expression  
XX construct, producing the binding domain-immunoglobulin fusion protein, a  
XX pharmaceutical composition comprising the binding domain-immunoglobulin  
XX fusion protein or polynucleotide and a carrier, and treating a subject  
XX having or suspected of having a malignant condition or a B-cell disorder.  
XX The binding domain-immunoglobulin fusion protein is useful for treating a  
XX subject having or suspected of having a malignant condition or a B-cell  
XX disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
XX myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
XX sclerosis or autoimmune disease. The present sequence is a binding domain  
XX -immunoglobulin fusion protein-associated protein sequence. Note: The  
XX sequence data for this patent formed part of the printed specification  
XX and is also available in electronic format directly from USPTO at  
XX seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not  
XX identified the sequences in the printed specification by their SEQ ID  
XX number therefore none of the sequences can be explicitly identified.  
XX  
XX Sequence 109 AA;  
XX  
XX Query Match 93.3%; Score 542; DB 7; Length 109;  
XX Best Local Similarity 95.3%; Pred. No. 7.8e-48;  
XX Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX 4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 63  
XX : |||||  
XX 4 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 63

QY 64 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPSSIEKTIKAK 109  
Db |||||  
64 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPAPIEKTISKAK 109  
  
RESULT 6  
AAR27680  
ID AAR27680 standard; protein; 110 AA.  
XX  
AC AAR27680;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAR-1993 (first entry)  
XX  
DE Human immunoglobulin IgG1 CH2 region.  
XX  
KW Isoallotype; IgG1 Glm(1,2,17); anti-allotype response; humanised Ab.  
XX  
OS Homo sapiens.  
XX  
PN WO9216562-A1.  
XX  
PD 01-OCT-1992.  
XX  
PF 12-MAR-1992; 92WO-GB000445.  
XX  
PR 12-MAR-1991; 91GB-00005245.  
XX  
PA (LYNX-) LYNXVALE LTD.  
XX  
PI Clark MR;  
XX  
DR WPI; 1992-349162/42.  
XX  
PT Humanised antibodies having modified allotypic determinant - useful for  
XX matching allotypes in therapy with decreased likelihood of causing  
XX undesirable immune responses.  
XX  
PS Disclosure; Fig 4c; 57pp; English.  
XX  
CC In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17.  
CC The inventor's propose eliminating these allotypes by amino acid changes  
CC to agree with the sequences of IG32, IG3 and IG4. None of the allotype  
CC sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes"  
CC should be suitable for therapeutic use in all patients. See AAR27678-  
CC R27681. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 110 AA;  
XX  
XX Query Match 93.3%; Score 542; DB 2; Length 110;  
XX Best Local Similarity 95.3%; Pred. No. 7.9e-48;  
XX Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 63  
Db : |||||  
5 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 64  
  
QY 64 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPSSIEKTIKAK 109  
Db |||||  
65 QYNSTYRVVSVLTVTLQDWLNKGKEYKCKVSNKGLPAPIEKTISKAK 110  
  
RESULT 7  
AAR41684  
ID AAR41684 standard; protein; 110 AA.  
XX  
AC AAR41684;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-OCT-1993 (first entry)  
XX  
XX Undefined ORF2 encoded by pAH4602.

XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;  
 KW chain; variable; constant; region; anti-human; transferrin; receptor;  
 KW antibody; brain; capillary; endothelial cell; conjugate;  
 KW neuropharmacological; diagnostic; agent; tumour; AIDS; stroke; epilepsy;  
 KW Parkinsons disease; Alzheimers disease.  
 XX Synthetic.  
 XX WO9310819-A1.  
 XX 10-JUN-1993.  
 XX 24-NOV-1992; 92WO-US010206.  
 XX 26-NOV-1991; 91US-00800458.  
 XX (ALKE-) ALKERMES INC.  
 XX Friden PM;  
 XX WPI; 1993-196742/24.  
 XX N-PSDB; AAQ43844.  
 XX Antibody conjugates specific for transferrin receptor - used for  
 PT diagnosis and treatment of cancer, AIDS and neurological disorders.  
 XX Disclosure; Fig 11K; 151pp; English.  
 CC The sequences given in A941682-85 are encoded by the expression vector,  
 CC pAH4602. This vector contains open reading frames encoding the heavy  
 CC chain variable region (VH) of the antibody 128.1, an ampicillin  
 CC resistance gene and a histidine (histidinol) selection marker.  
 CC Transcription of the VH gene is from the VH promoter of the murine 27.44  
 CC gene. The vector also includes a heavy chain immunoglobulin enhancer and  
 CC the human gammal constant region (CH). The VH region of 128.1 was  
 CC isolated by polymerase chain reaction and cloned into plasmid pAH4274.  
 CC This was achieved by digesting the plasmid and the product with EcoRV and  
 CC NheI. The VH gene was inserted in-frame with the human gammal CH region  
 CC CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an  
 CC anti-human transferrin receptor antibody which binds to the transferrin  
 CC receptor on brain capillary endothelial cells. This antibody may be used  
 CC in a conjugate in which it is linked to a neuro-pharmaceutical or  
 CC diagnostic agent. The conjugate may be used to treat or prevent  
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 110 AA;  
 SQ  
 Query Match 93.3%; Score 542; DB 2; Length 110;  
 Best Local Similarity 95.3%; Pred. No. 7.9e-48;  
 Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREE 63  
 : |||||  
 Db 5 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREE 64  
 QY 64 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109  
 : |||||  
 Db 65 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 110  
 RESULT 8  
 ADH75385  
 ID ADH75385 standard; protein; 110 AA.  
 XX AC ADH75385;  
 XX 22-APR-2004 (first entry)  
 XX Human IgG1 CH2 region.  
 DE  
 XX  
 KW Polymoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;  
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;  
 KW allergic disease.  
 XX Homo sapiens.  
 XX US5965709-A.  
 XX 12-OCT-1999.  
 XX 21-APR-1994; 94US-00232539.  
 XX 14-AUG-1991; 91US-00744768.  
 KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
 KW autoimmune disease; human; IgG; immunoglobulin.  
 XX Homo sapiens.  
 XX US2004002587-A1.  
 XX 01-JAN-2004.  
 XX 20-FEB-2003; 2003US-00370749.  
 XX 20-FEB-2002; 2002US-0358161P.  
 XX (WATK/) WATKINS J D.  
 XX (ALLA/) ALLAN B.  
 XX Watkins JD, Allan B;  
 XX WPI; 2004-070755/07.  
 XX New composition comprising a variant of a parent polypeptide having at  
 PT least a portion of a Fe region, useful in treating e.g., autoimmune  
 PT diseases.  
 XX Claim 20; SEQ ID NO 23; 62pp; English.  
 PS The invention relates to a new composition comprises a variant of a  
 CC parent polypeptide having at least a portion of a Fe region. The variant  
 CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the  
 CC presence of effector cells more effectively than the parent polypeptide  
 CC and comprises at least one amino acid modification at position 280 in the  
 CC Fc region. The composition is useful in treating diseases e.g.,  
 CC autoimmune diseases. The present sequence represents the amino acid  
 CC sequence of a human immunoglobulin G, IgG, CH region.  
 XX Sequence 110 AA;  
 SQ  
 Query Match 93.3%; Score 542; DB 8; Length 110;  
 Best Local Similarity 95.3%; Pred. No. 7.9e-48;  
 Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREE 63  
 : |||||  
 Db 5 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNKTKPREE 64  
 QY 64 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109  
 : |||||  
 Db 65 QYNSTYRVWSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 110  
 RESULT 9  
 AAY42626  
 ID AAY42626 standard; protein; 105 AA.  
 XX AC AAY42626;  
 XX 10-JAN-2000 (first entry)  
 XX Human IgG1 Fc gamma2 residues.  
 XX Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;  
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;  
 KW allergic disease.  
 XX Homo sapiens.  
 XX US5965709-A.  
 XX 12-OCT-1999.  
 XX 21-APR-1994; 94US-00232539.  
 XX 14-AUG-1991; 91US-00744768.







Qy		64 QYNSTYRWVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109 
Db		65 QYNSTYRWVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 110 

RESULT 14  
ADL90103  
ID ADL90103 standard; protein; 110 AA.

RESULT 15  
ADH75413  
ID ADH75413 standard; protein; 110 AA.  
XX  
AC ADH75413;  
XX  
DT 23-APR-2004 (first entry)

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:37:49 ; Search time 16.4247 Seconds  
(without alignments)  
638.529 Million cell updates/sec

Title: US-09-674-857-1  
Perfect score: 581  
Sequence: 1 APPVAGSFLFPKPKDTL.....CKVSNKGLPSSIEKTISKAK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 44790

Minimum DB seq length: 0  
Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: Pirl:.\*  
2: Pirl:.\*  
3: Pirl:.\*  
4: Pirl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276	47.5	88	A30503	Ig gamma-2b chain
2	141	24.3	107	I68726	IgE chain C3 regio
3	139	23.9	106	K3HU	Ig kappa chain C r
4	138	23.8	107	I68730	IgE chain C3 regio
5	134	23.1	99	S26653	Ig kappa chain C r
6	133.5	23.0	105	B30554	Ig lambda chain C
7	132	22.7	103	B26167	Ig lambda chain C
8	131.5	22.6	105	B26434	Ig lambda-5 chain
9	130	22.4	110	S43147	Ig upsilon chain -
10	127.5	21.9	105	L1MS	Ig lambda-1 chain
11	127.5	21.9	106	S22760	Ig lambda-2 chain
12	126.5	21.8	106	S00259	Ig lambda-5 chain
13	118.5	20.4	105	L2HU	Ig lambda chain C
14	118.5	20.4	105	H32529	Ig lambda chain C
15	117.5	20.2	98	S26654	Ig lambda chain C
16	116.5	20.1	104	P53275	Ig kappa-1 chain C
17	115	19.8	99	A37927	Ig kappa chain C r
18	114	19.6	102	B34509	Ig light chain C r
19	113.5	19.5	102	L7RB	Ig lambda chain C
20	112.5	19.4	103	K4RB	Ig kappa-B4 chain
21	110	18.9	106	I50741	Ig lambda chain -
22	110	18.9	106	I50740	Ig lambda chain C
23	108.5	18.7	105	L1PG	Ig lambda chain C
24	108	18.6	105	A27390	Ig lambda-1 chain
25	107	18.4	106	K1MS	Ig kappa chain C r
26	104	17.9	104	K5RBV	Ig kappa chain C r
27	102.5	17.6	102	I46731	lambda-chain C-reg
28	99	17.0	105	B27390	Ig lambda-2 chain
29	99	17.0	106	K1RTB	Ig kappa chain C r

30	99	17.0	106	1	K4RBBS	Ig kappa-2 chain C
31	99	17.0	106	2	G20907	Ig kappa-B4 chain
32	94	16.2	104	1	L3MS	Ig lambda-3 chain
33	94	16.2	105	2	S22762	Ig lambda-2 chain
34	94	16.2	106	1	K1RTA	Ig kappa chain C r
35	93	16.0	104	1	K9RB	Ig kappa-B9 chain
36	92	15.8	103	1	K5RB	Ig kappa-B5 chain
37	85	14.6	97	2	S26652	Ig gamma-1 chain C
38	83.5	14.4	78	2	C34509	Ig light chain C r
39	80	13.8	82	2	I57802	Ig lambda2-like ch
40	80	13.8	104	1	L2MS	Ig lambda-2 chain
41	80	13.8	105	2	S22759	Ig lambda-2 chain
42	79.5	13.7	78	2	D34509	Ig light chain C r
43	76.5	13.2	67	2	PL0186	Ig lambda chain. C
44	64.5	11.1	107	2	I68725	IgE chain C2 regio
45	64	11.0	90	2	A24629	Ig gamma-3 chain C

ALIGNMENTS

RESULT 1

A30503 Ig gamma-2b chain C region (B5.7A12) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C;Accession: A30503  
R;Gilmore, G.L.; Bard, J.A.; Birshstein, B.K.  
J. Immunol. 141, 1754-1761, 1988  
A;Title: DNA rearrangements affecting both variable and constant regions of Ig H chain g  
A;Reference number: A30503; MUID:88315788; PMID:2842402  
A;Accession: A30503  
A;Molecule type: mRNA  
A;Residues: 1-88 <GIL>  
A;Cross-references: GB:M21925  
A;Experimental source: myeloma cell line MPC11  
A;Note: the authors translated the codon GAG for residue 41 as Ser  
C;Genetics:  
A;Introns: 46/3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-70/Domain: immunoglobulin homology <IMM>

Query Match 47.5%; Score 276; DB 2; Length 88;  
Best Local Similarity 63.2%; Pred. No. 2.1e-20;  
Matches 48; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy	23	SRTPEVTCVVVDYSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVTLQHDW	82
Db	1	SLTPKVTCTVVVDVSDDDPDVQISWVFNNVSEEVHFAQTQTTHREDYNTIRVSVSTLPIQHODW	60
Qy	83	LNQKEYKCKVSNKGLP	98
Db	61	MSGKEFKCKVNNKDL	76

RESULT 2

I68726 IgE chain C3 region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
C;Accession: I68726  
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.  
Immunogenetics 27, 288-292, 1988  
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s  
A;Reference number: I54443; MUID:88152907; PMID:3346043  
A;Accession: I68726  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-107 <RES>  
A;Cross-references: GB:M22930; NID:gl94455; PIDN:AAA37911.1; PID:gl94460  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;22-90/Domain: immunoglobulin homology <IMM>



```

Db      6 GVITLPPSLD-LYQNGAPKLTCLVVDLSEKKNVNTWQEKTSVSASQWY---TKH 61
Qy      54 HNAKTKPREQYNTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 107
Db      62 HN-----NATTSITSLPVAKDWISGYGVCIVDHPDFPKPIVRSITK 105

RESULT 5
S26653
Ig kappa chain C region - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S26653
R:Erlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A:Reference number: S26652; MUID:91355693; PMID:2129418
A:Accession: S26653
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-99 <EHR>
A:Cross-references: EMBL:X65287
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match      23.1%; Score 134; DB 2; Length 99;
Best Local Similarity 33.3%; Pred. No. 2.7e-06;
Matches 34; Conservative 20; Mismatches 42; Indels 6; Gaps 3;

Qy      4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG--EVHNAKTKPR 61
Db      2 VAAPSVEIFP--PSDEQLKSGTASVCLLNFFPR--EAKYQWKVDNALQSGNSQESVTE 57

Qy      62 EQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEK 103
Db      58 QDSKDSYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTK 99

RESULT 6
B30554
Ig lambda chain C region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30554
R:Poley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A:Reference number: A30554; MUID:89093962; PMID:2492052
A:Accession: B30554
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-105 <FOL>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:20-88/Domain: immunoglobulin homology <IMM>

Query Match      23.0%; Score 133.5; DB 2; Length 105;
Best Local Similarity 30.6%; Pred. No. 3.2e-06;
Matches 33; Conservative 22; Mismatches 46; Indels 7; Gaps 4;

Qy      3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61
Db      2 PKSAPSVTLFPSPKEE--LDTNKATVCLISD--FYFGSVNVVWKADGSIINQNVKTQA 57

Qy      62 EQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 109
Db      58 SKQSNKYAASVLTLTGSEWKSSTCEVTHG--STVTKTVKPSE 103

RESULT 7
B26167
Ig lambda chain C region - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B26167
R:Parvari, R.; Ziv, B.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
A:Title: Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germi
A:Reference number: A26167; MUID:87218480; PMID:3107981
A:Accession: B26167
A:Molecule type: mRNA; DNA
A:Residues: 1-103 <PAR>
A:Cross-references: UNIPROT:P20763; GB:M333049
A:Note: 90-Asp was found in one cDNA clone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-87/Domain: immunoglobulin homology <IMM>

Query Match      22.7%; Score 132; DB 2; Length 103;
Best Local Similarity 29.9%; Pred. No. 4.4e-06;
Matches 32; Conservative 25; Mismatches 44; Indels 6; Gaps 5;

Qy      3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
Db      2 PKVAPTITLPPPS-KEELNEATKATLVCLINDP-YPSP-VTVDWVIDG-STRSETTAPQ 57

Qy      63 EQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 109
Db      58 RQSNQYMASSVLSLSASDSSSHETVTCRVTHG--TSITKTLKRSE 102

RESULT 8
B26434
Ig lambda-5 chain C region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C:Accession: B26434
R:Sakaguchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A:Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lympho
A:Reference number: A26434; MUID:87065143; PMID:3024017
A:Accession: B26434
A:Molecule type: mRNA
A:Residues: 1-105 <SAK>
A:Cross-references: GB:M30387
A:Note: the authors translated the codon TAC for residue 84 as Thr
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      22.6%; Score 131.5; DB 2; Length 105;
Best Local Similarity 32.4%; Pred. No. 5e-06;
Matches 35; Conservative 25; Mismatches 41; Indels 7; Gaps 5;

Qy      3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
Db      2 PKSDPLVTLFLPSLKN-LQPTR-PQLVCLVSE--FPGTLVDVNDKVDGVPVTOGVETQP 57

Qy      62 EQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 109
Db      58 SKQTNNKYVSVSYLTLSLDQMPHSRYSCRVTHEG--NTVEKSVSPA 103

RESULT 9
S43147
Ig upsilon chain - duck (fragment)
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C:Accession: S43147
R:Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
submitted to the EMBL Data Library, March 1994
A:Description: Evidence from duck immunoglobulin genes that Igy is the common ancestor o
A:Reference number: S43145
A:Accession: S43147
A:Status: preliminary
```

A;Molecule type: DNA  
A;Residues: 1-110 <MAG>  
A;Cross-references: EMBL:X78355; NID:g468612; PID:g468613  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match	22.4%;	Score 130;	DB 2;	Length 110;
Best Local Similarity	28.4%;	Pred. No. 7.5e-06;		
Matches	31;	Conservative	22;	Mismatches 48; Indels

Qy	5	AGP-----SVFLFPKPKD	TL	SI	ST	PT	VT	CV	VD	VS	HD	EV	KF	NV	YD	GV	VH	NA	KT	58	
Db	2	SGFQSCPTQIFVVP	PSP	-	GS	LI	RO	DA	KV	HL	LN	LP	-	SD	AS	LS	IS	WT	RE	KS	59
Qy	59	KPREQYNSTYR	VV	SV	LV	LV	LD	QW	LK	GE	YK	CK	VN	KN	GL	PS	IE	KT	IS	107	
Db	60	MVLTEHFNQ	TFT	ASS	LS	AI	ST	OD	W	LAG	E	FT	CT	VO	HE	DL	PE	PL	GK	SI	108

RESULT 10

L1M5  
 Ig lambda-1 chain C region - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 31-Mar-1981 #sequence revision 29-Jun-1981 #text\_change 09-Jul-2004  
 C/Accession: A93922; A93251; A93282; A93775; A02126  
 R/Salsing, E.; Miller, J.; Wilson, R.; Storb, U.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 4681-4685, 1982  
 A/Title: Evolution of mouse immunoglobulin lambda genes.  
 A/Reference number: A93922; MUID: 83014953; PMID: 6812053  
 A/Accession: A93922  
 A/Molecule type: DNA  
 A/Residues: 1-105 <SFL>  
 A/Cross-references: UNIPROT:P01843; GB:J00587; NID:g197754; PIDN:AA859672.1; PID:g197761  
 R/Bothwell, A.L.M.; Paskind, M.; Schwartz, R.C.; Sonenshein, G.E.; Geiter, M.L.; Baltimore, D.  
 Nature 290, 65-67, 1981  
 A/Title: Dual expression of lambda genes in the MOPC-315 plasmacytoma.  
 A/Reference number: A93251; MUID: 81148806; PMID: 6259534  
 A/Contents: MOPC 315  
 A/Accession: A93251  
 A/Molecule type: DNA  
 A/Residues: 1-105 <BOL>  
 A/Cross-references: GB:J00582; NID:g197595; PIDN:AA51636.1; PID:g197598  
 A/Note: the sequence was determined from an abnormal differentiated gene  
 A/Note: the MOPC 315 cell line produces two light chains, one normal lambda-2 chain and  
 one completely normal  
 R/Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.  
 Nature 298, 380-382, 1982  
 A/Title: Somatic variants of murine immunoglobulin lambda light chains.  
 A/Reference number: A93282; MUID: 82220143; PMID: 6283385

Query Match 21.9%; Score 127.5; DB 1; Length 105;  
Best Local Similarity 30.8%; Pred. NO. 1.3e-05;  
Matches 33; Conservative 19; Mismatches 48; Indels 7; Gaps 3;

Qy	3	PVAGPSVFLPPKPKD	TLMISTPEVTCVWDVSHEDPEVKFNKVVGDVEV--HNAKTRP	61
Db	2	PKSPSVTLTLPSPSSE	-----ETNKATLTCTITDFYPGVTVDMKVDGTFVTOGMETTP	57
Qy	62	EEQYNSTYRWVSVLT	VHLQDWLNGKEYKCKVSNKGLPSSIEKTI	108
Db	58	SKGSNNKYMASVYLT	ATARAWRHSSYSCQVTHEG--HTVEKSLGRA	102

RESULT 11

S22760  
IG lambda-2 chain C region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
C:Accession: S22760  
R:Weiss, S.; Wu, G.E.  
EMBO J. 6, 927-932, 1987  
A:title: Somatic point mutations in unrearranged immunoglobulin gene segments  
A:reference number: S22759; MUID:87246527; PMID:3109891

Query Match	21.9%	Score	127.5;	DB 2;	Length	106;			
Best Local Similarity	30.8%;	Pred. No.	1.3e-05;						
Matches	33;	Conservative	19;	Mismatches	48;	Indels	77;	Gaps	3;

Qy	3	PNVAGPSVFLPPKPKD	TLMI	STPEVTCVVDV	SHDEPVEN	KNYVDG	VEV	HNAAK	TPR	61
Db	3	PKXSSVTLVFLPPSS	EL---	ETNAK	TLCTIT	DFYPGV	VTVD	MKDPVT	QGMET	58
Qy	62	BEQYNSTYRV	VSVL	VLH	QDNL	WGKEYCK	RVSN	KGLP	SI	108
Db	59	SKQSNKNTY	MASS	LYLT	LTAR	WERH	SSYSC	QVTH	EG--	103

RESULT 12

S00259  
Ig lambda-5 chain C region - western wild mouse  
C:Species: Mus spretus (western wild mouse)  
C:Date: 31-Dec-1988 #sequence\_revision 07-Sep-1990 #text\_change 21-Jan-2000  
C:Accession: S00259  
R:Mami, F.; Cazenave, P.A.; Kindt, T.J.  
EMBO J. 7, 117-122, 1988  
A:Title: Conservation of the immunoglobulin C-lambda-5 gene in the Mus genus.  
A:Reference number: S00259; MUID:88196070; PMID:3129289  
A:Accession: S00259  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-106 <MAM>  
A:Note: the sequence was translated from the germline gene  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-49/Domain: immunoglobulin homology <IMM>

Query Match	21.8%	Score 126.5;	DB 2;	Length 106;
Best Local Similarity	30.6%	Pred. No. 1.6e-05;		
Matches 33;	Conservative 23;	Mismatches 45;	Indels 47;	Gaps 3;

[illegible]

## RESULT 13

L2HU  
Ig lambda chain C regions - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1991 #sequence revision 31-Jan-1981 #text change 09-Jul-2004  
C:Accession: A92057; A90243; A91970; A91650; A90375; B90381; A93268; A02125  
R:Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 245, 2171-2176, 1970  
A:Title: The amino acid sequence of a lambda type Bence-Jones protein Sh  
A:Reference number: A92057; MUID:70166723; PMID:4909564  
A:Contents: Bence Jones protein Sh  
A:Accession: A92057  
A:Molecule type: protein  
A:Residues: 1-105 <TIT>  
A:CROSS-references: UNIPROT:P01842  
R:Milstein, C.; Clegg, J.B.; Jarvis, J.M.  
Biochem. J. 110, 631-652, 1968  
A:Title: Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jones  
A:Reference number: A90243; MUID:69088380; PMID:4883841  
A:Contents: Bence Jones protein X; disulfide bonds  
A:Accession: A90243  
A:Molecule type: protein  
A:Residues: 1-105 <MIL>  
R:Kamerling, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.  
J. Biochem. 93, 421-429, 1983  
A:Title: Comparative studies on the structure of the light chains of human immunoglobulin  
A:Reference number: A91970; MUID:83186114; PMID:6404900  
A:Contents: Bence-Jones protein Nig-64  
A:Accession: A91970  
A:Molecule type: protein  
A:Residues: 1-105 <KAM>  
R:Ponstingl, H.; Hess, M.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 352, 247-266, 1971  
A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom lambda-Typ, Su  
A:Reference number: A91650; MUID:71150336; PMID:5549558  
A:Contents: Bence Jones protein Kern  
A:Accession: A91650  
A:Molecule type: protein  
A:Residues: 1-44, 'G', 46-105 <PON>  
A:Note: this sequence has the Kern+ marker, 45-Gly (instead of Ser)  
R:Chen, B.L.; Poljak, R.J.  
Biochemistry 13, 1295-1302, 1974  
A:Title: Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobul  
A:Reference number: A90375; MUID:74109253; PMID:4814727  
A:Contents: myeloma protein Newm; partial sequence  
A:Accession: A90375  
A:Molecule type: protein  
A:Residues: 1-81, 'K', 83-105 <CHE>  
A:Note: this chain has the Oz+ marker, 82-Lys (instead of Arg)  
R:Poljak, R.J.; Amzel, L.M.; Avey, H.P.; Chen, B.L.; Phizackerley, R.P.; Saul, F.  
Proc. Natl. Acad. Sci. U.S.A. 71, 3440-3444, 1974  
A:Title: The three-dimensional structure of the Fab' fragment of a human myeloma immunog  
A:Reference number: A93788; MUID:75046825; PMID:4215080  
A:Contents: annotation; Newm; X-ray crystallography, 2.0 angstroms  
R:Fett, J.W.; Deutsch, H.F.  
Biochemistry 13, 4102-4114, 1974  
A:Title: Primary structure of the Mcg lambda chain.  
A:Reference number: A90381; MUID:75013804; PMID:4415202  
A:Contents: Bence Jones protein Mcg; partial sequence  
A:Accession: B90381  
A:Molecule type: protein  
A:Residues: 1-4, 'N', 6, 'T', 8-44, 'G', 46-55, 'K', 57-105 <FET>  
A:Note: this sequence has the Kern+ marker, 45-Gly, and the Mcg+ marker, 5-Asn, 7-Thr, a  
R:Edmondson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.  
Biochemistry 14, 3953-3961, 1975  
A:Title: Rotational allomerism and divergent evolution of domains in immunoglobulin light  
A:Reference number: A90391  
A:Contents: annotation; Mcg; X-ray crystallography, 2.3 angstroms  
R:Hieter, P.A.; Hollis, G.F.; Korsmeyer, S.J.; Waldmann, T.A.; Leder, P.  
Nature 294, 536-540, 1981  
A:Title: Clustered arrangement of immunoglobulin lambda constant region genes in man.  
A:Reference number: A93268; MUID:82080680; PMID:6273747  
A:Accession: A93268

A:Molecule type: DNA  
A:Residues: 1-105 <HIE>  
A:CROSS-references: GB:J00253; NID:gi86118; PIDN:AAA59107.1; PID:gi86127  
A:Note: six tandem lambda-type genes were identified and the three most 5' were sequence  
ce (lambda-3)  
C:Comment: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins Sh, X, and N  
C:Genetics:  
A:Gene: GDB:IGLC2; IGLC  
A:CROSS-references: GDB:120691; OMIM:147220  
A:Map position: 22q11.2-22q11.2  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer  
F;20-88/Domain: immunoglobulin homology <IMM>  
F;27-86/Disulfide bonds: #status experimental  
F;104/Disulfide bonds: interchain (to heavy chain) #status experimental  
Query Match 20.4%; Score 118.5; DB 1; Length 105;  
Best Local Similarity 28.6%; Pred. No. 9.7e-05;  
Matches 30; Conservative 23; Mismatches 45; Indels 7; Gaps 4;  
QY 3 PVAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61  
DB 2 PKAAPSVTLFPPSSE--LQANKATLVCLISD--FYPGAVTVAKADSSPVKAGVETTP 57  
QY 62 EEQYNSTYRVVSVLTVTLQHDWLNKGEYKCKVSNKGLPSSIEKTIS 106  
DB 58 SKQSNKYAAASSYLSLTPEQMKSHRSYSCQVTHEG--STVEKTV 100  
RESULT 14  
H32529  
Ig lambda chain C region (clone pDH2) - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: H32529  
R:Hayzer, D.J.; Duvoisin, R.M.; Jaton, J.C.  
Biochem. J. 245, 691-697, 1987  
A:Title: cDNA clones encoding rabbit immunoglobulin lambda chains. Evidence for length v  
A:Reference number: A90338; MUID:88024122; PMID:3117050  
A:Accession: H32529  
A:Molecule type: mRNA  
A:Residues: 1-105 <HAY>  
A:CROSS-references: GB:M25620; NID:G294487; PIDN:AAA75092.1; PID:G561834  
A:Note: the authors translated the codon GTC for residue 84 as Thr and ACC for residue 8  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;20-88/Domain: immunoglobulin homology <IMM>  
Query Match 20.4%; Score 118.5; DB 2; Length 105;  
Best Local Similarity 28.7%; Pred. No. 9.7e-05;  
Matches 31; Conservative 21; Mismatches 49; Indels 7; Gaps 4;  
QY 3 PVAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61  
DB 2 PAVTPSVILFPPSSEE--LKDNKATLVCLIND--FYPGTVKVKNKADGTPVTOGVDTPQ 57  
QY 62 EEQYNSTYRVVSVLTVTLQHDWLNKGEYKCKVSNKGLPSSIEKTISKAK 109  
DB 58 SKQSNKYAAASSFLSLSANQWKSYQSVTCVTHEG--HTVEKSLAPAE 103  
RESULT 15  
S26654  
Ig lambda chain C region - chimpanzee (fragment)  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 19-Mar-1997 #sequence revision 18-Jul-1997 #text\_change 21-Jan-2000  
C:Accession: S26654  
R:Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybridomas 1, 23-26, 1990  
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
A:Reference number: S26652; MUID:91355693; PMID:2129418

A;Accession: S26654  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-98 <EHR>  
A;Cross-references: EMBL:X65286  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-88/Domain: immunoglobulin homology <IMM>

Query Match	20.2%	Score 117.5;	DB 2;	Length 98;
Best Local Similarity	30.1%	Pred. No. 0.00011;		
Matches	31;	Conservative 20;	Mismatches 45;	Indels 7; Gaps 4;
QY	3	PVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR	61	
Db	2	PKAAPSVTLFPPSBE--LQANKATLVCLISD--FYPGAVTVAKADSSPVKAGVETTP	57	
QY	62	EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKT	104	
Db	58	SKQSNKNYAASSYLSLTPEQWKSHKYSYCOVTHEG--STVEKT	98	

Search completed: November 17, 2005, 07:55:07  
Job time : 17.4247 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.1461 Seconds  
(without alignments)  
723.518 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVLPFPKPKDTL.....CKVSNKGLPSSIEKTIKAK 109

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	139	23.9	106	1	KAC_HUMAN	P01834 homo sapien
2	132	22.7	103	1	LAC_CHICK	P20763 gallus gall
3	127.5	21.9	105	1	LAC1_MOUSE	P01843 mus musculus
4	126.5	21.8	105	1	LAC5_MUSSP	P20765 mus musculus
5	122.5	21.1	105	1	LAC5_MOUSE	P20764 mus musculus
6	121.5	20.9	106	2	O8TCJ5	O8TCJ5 homo sapien
7	118.5	20.4	105	1	LAC_HUMAN	P01842 homo sapien
8	113.5	19.5	105	1	LAC_RABIT	P01847 oryctolagus
9	112.5	19.4	103	1	KAC4_RABIT	P01840 oryctolagus
10	108.5	18.7	105	1	LAC_PIG	P01846 sus scrofa
11	108	18.6	104	1	LAC1_RAT	P20766 rattus norv
12	107	18.4	106	1	KAC_MOUSE	P01837 mus musculus
13	104	17.9	104	1	KAC6_RABIT	P03984 oryctolagus
14	99	17.0	104	1	LAC2_RAT	P20767 rattus norv
15	99	17.0	106	1	KACB_RABIT	P01839 oryctolagus
16	99	17.0	106	1	KACB_RAT	P01835 rattus norv
17	94	16.2	104	1	LAC3_MOUSE	P01845 mus musculus
18	94	16.2	106	1	KAC3_RAT	P01836 rattus norv
19	93	16.0	104	1	KAC5_RABIT	P01838 oryctolagus
20	92	15.8	103	1	KAC5_RABIT	P01841 oryctolagus
21	80	13.8	104	1	LAC2_MOUSE	P01844 mus musculus
22	80	13.8	105	2	O99JC1	O99JC1 mus musculus
23	66	11.4	107	2	O8KVI0	O8KVI0 bacillus an
24	65	11.4	107	2	O6EZI5	O6EZI5 bacillus an
25	63	10.8	98	2	O7XZF9	O7XZF9 oryza sativ
26	62	10.7	93	2	O6LBV9	O6LBV9 mus musculus
27	61.5	10.6	93	2	O6LBW2	O6LBW2 mus musculus
28	61	10.5	91	2	O9JKP1	O9JKP1 marmota mon
29	60.5	10.4	74	2	P79659	P79659 oncorhynch
30	60.5	10.4	74	2	P79660	P79660 oncorhynch
31	60	10.3	73	2	O8FBY4	O8FBY4 escherichia

32	59	10.2	79	1	SN5P_HUMAN	P00697 homo sapien
33	59	10.2	91	2	Q31248	Q31248 peromyscus
34	59	10.2	93	2	Q31158	Q31158 mus musculus
35	58.5	10.1	55	2	Q768W8	Q768W8 uncultured
36	58.5	10.1	93	2	O19471	O19471 mus musculus
37	58.5	10.1	93	2	O19472	O19472 mus musculus
38	58.5	10.1	93	2	Q9QUH8	Q9QUH8 mus musculus
39	58	10.0	103	2	Q8HX76	Q8HX76 sus scrofa
40	58	10.0	104	2	Q8CST6	Q8CST6 mus musculus
41	58	10.0	106	2	Q31261	Q31261 rattus norv
42	57.5	9.9	55	2	Q768W5	Q768W5 uncultured
43	57.5	9.9	65	1	DN71L_SULAC	P13123 sulfolobus
44	57.5	9.9	95	1	DAFT_TRYCR	Q26327 trypanosoma
45	57	9.8	90	1	ALB2_SULTO	Q97116 sulfolobus

#### ALIGNMENTS

RESULT 1  
KAC\_HUMAN  
ID KAC\_HUMAN STANDARD; PRT; 106 AA.  
AC P01834;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain C region.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE (MYELOMA PROTEIN EU).  
RX MEDLINE=71064023; PubMed=5489770;  
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";  
RL Biochemistry 9:3155-3161(1970).  
RN [2]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [3]  
RP SEQUENCE (BENCE-JONES PROTEIN TI).  
RX MEDLINE=72188439; PubMed=5027703;  
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;  
RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;  
RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";  
RL Cell 22:197-207(1980).  
RN [5]  
RP SEQUENCE (BENCE-JONES PROTEIN ROY).  
RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;  
RL (in) Franek F., Shugar D. (eds.);  
Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).  
RN [6]  
RP SEQUENCE (BENCE-JONES PROTEIN CUM).  
RX MEDLINE=68242259; PubMed=5586923;  
RA Hilschmann N.;

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).

RN [7]

RP SEQUENCE (BENCE-JONES PROTEIN AG).

RX MEDLINE=69234734; PubMed=4893682;

RA Titani K., Shinoda T., Putnam F.W.;

RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";

RL J. Biol. Chem. 244:3550-3560(1969).

RN [8]

RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).

RX MEDLINE=70201507; PubMed=5447531;

RA Kohler H., Shimizu A., Paul C., Putnam F.W.;

RT "Macroglobulin structure: variable sequence of light and heavy chains.";

RL Science 169:56-59(1970).

RN [9]

RP SEQUENCE OF 1-33; 38-41 AND 62-80.

RC TISSUE=Abdominal adipose tissue;

RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;

RA Olsen K.E., Sletten K., Westermarck P.;

RT "Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";

RL Biochem. Biophys. Res. Commun. 245:713-716(1998).

CC -1- MISCELLANEOUS: The EU sequence has the INV (3) allotypic marker, Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic marker, Ala-45 and Leu-83.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -----

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CC -----

DR EMBL; J00241; AAA58989.1; -.

DR PIR; B90562; K3HU.

DR PDB; 1DSB; X-ray; A/L=1-103.

DR PDB; 1DS1; X-ray; L=1-103.

DR PDB; 1D6V; X-ray; L=1-103.

DR PDB; 1HEZ; X-ray; -.

DR PDB; 1HKL; X-ray; L=1-106.

DR PDB; 1I7Z; X-ray; A/C=1-106.

DR PDB; 1MIM; X-ray; L=1-105.

DR Genew; HGNC:5716; IGKC.

DR DR InvDB; HIX0021121; -.

DR MIM; 147200; -.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig\_LIKE.

DR PROSITE; PS00835; IG\_LIKE; 1.

DR PROSITE; PS00290; IG\_MHC; 1.

KW 3D-structure: Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.

KW NON\_TER 1 1

FT DOMAIN 5 102 Ig-like.

FT DISULFID 26 86

FT VARIANT 106 106 Interchain (with a heavy chain).

FT VARIANT 83 83 /FTId=VAR\_003897.

FT D-> N (in INV(1,2) marker).

FT E -> Q (in Ref. 5 and 6).

FT CONFLICT 14 14

FT CONFLICT 57 57

FT STRAND 3 3

FT STRAND 6 10

FT HELIX 14 17

FT TURN 18 20

FT STRAND 21 32

FT STRAND 37 42

FT TURN 43 44

FT STRAND 45 47

FT STRAND 51 55

FT TURN 60 62

FT STRAND 65 74

FT HELIX 75 79

FT TURN 80 80

FT STRAND 83 89

FT TURN 91 92

FT STRAND 97 102

FT TURN 103 104

SQ SEQUENCE 106 AA; 51984D1PDD372CE8 CRC64;

Query Match 23.9%; Score 139; DB 1; Length 106;

Best Local Similarity 31.5%; Pred.No. 6.2e-06;

Matches 34; Conservative 24; Mismatches 44; Indels 6; Gaps 3;

QY 4 VAGPSVFLPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG--EVFNAKTKPR 61

DB 2 VAAPSVFIFP--PSDQLKSGTASVVCLLNNFYP--EAKVQKVDNALQSGNSQESVTE 57

QY 62 BEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109

DB 58 QDSKSTYLSSTLTLSKADYKKHVKYACEVTHQGLSPVTKSFNRGE 105

RESULT 2

LAC\_CHICK

ID LAC\_CHICK STANDARD; PRT; 103 AA.

AC P20763;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig lambda chain C region.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87218480; PubMed=3107981;

RA Parvari R., Ziv E., Lentrner F., Tel-Or S., Burstein Y., Schechter I.;

RT "Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus.";

RL EMBL J. 6:97-102(1987).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -----

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CC -----

DR EMBL; X04768; CAA28461.1; -.

DR PIR; B26167; B26167.

DR HSSP; P01842; 7FAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_c1.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00407; IGc1; 1.

DR PROSITE; PS00835; IG\_LIKE; 1.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Immunoglobulin C region; Immunoglobulin domain; Polymorphism.

KW NON\_TER 1 1

FT DOMAIN 6 99 Ig-like.

FT DISULFID 28 85

FT DISULFID 103 103 Interchain (with heavy chain).

FT VARIANT 90 90 N -> D.

FT SEQUENCE 103 AA; 11361 MW; 77BF341B511B91B2 CRC64;

```

Query Match      22.7%; Score 132; DB 1; Length 103;
Best Local Similarity 29.9%; Pred. No. 2.9e-05;
Matches 32; Conservative 25; Mismatches 44; Indels 6; Gaps 5;

QY 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 2 PKVAPTITLPPPS-KEELNEATKATLVCLINDF-YPSF-VTVVDVIG-STRGETTAPQ 57
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 63 EQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 58 RQNSQYMASSYLSLSASDWSHSHETTCRVTHNG-TSITKTKRSE 102
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 3
LAC1 MOUSE
ID LAC1 MOUSE STANDARD; PRT; 105 AA.
AC P01843;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; PubMed=6812053;
RA Selsing E., Miller J., Wilson R., Storb U.;
RT "Evolution of mouse immunoglobulin lambda genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685 (1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE=81148806; PubMed=6259534;
RA Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA Gelfer M.B., Baltimore D.;
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL Nature 290:65-67 (1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE=82220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382 (1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=71107854; PubMed=5276767;
RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:590-594 (1971).
CC -1- MISCCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
normal lambda-2 chain and 1 abnormal lambda-1 chain that is
missing a large part of the V region. The C region sequence (shown
here) appears completely normal.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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DB EMBL; J00582; AAAS1636.1; -
DB EMBL; J00587; AABS9672.1; -
DB PIR; A93922; LIMS.
DB PDB; 1JNH; X-ray; A=1-105.
DB InterPro; IPR007110; Ig-like.
DB InterPro; IPR003006; Ig_MHC.
DB Pfam; PF00047; Ig; 1.

DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 100 Ig-like.
FT DOMAIN 6 100
FT DISULFID 27 86 Interchain (with heavy chain).
FT DISULFID 104 104 ET -> TE (in Ref. 4).
FT CONFLICT 19 20 Q -> E (in Ref. 4).
FT CONFLICT 56 56 Missing (in Ref. 4).
FT CONFLICT 75 75 HS -> SH (in Ref. 4).
FT CONFLICT 81 82 S -> SS (in Ref. 4).
FT CONFLICT 85 85 E -> Q (in Ref. 4).
FT CONFLICT 96 96
FT STRAND 4 4
FT STRAND 7 7
FT STRAND 10 11
FT STRAND 15 19
FT HELIX 20 21
FT TURN 20 21
FT STRAND 22 33
FT STRAND 37 43
FT TURN 44 45
FT STRAND 46 48
FT STRAND 50 51
FT TURN 52 54
FT STRAND 58 60
FT TURN 61 63
FT STRAND 64 74
FT HELIX 75 80
FT STRAND 84 90
FT TURN 91 92
FT STRAND 93 99
SQ SEQUENCE 105 AA; 11575 MW; A89F2B09BCFCA018 CRC64;

Query Match      21.9%; Score 127.5; DB 1; Length 105;
Best Local Similarity 30.8%; Pred. No. 8.3e-05;
Matches 33; Conservative 19; Mismatches 48; Indels 7; Gaps 3;

QY 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 2 PKSSPSVTLFPPPSSEEL---ETNKATLVCTITDFYPGVTVVDKVDGTPVTQGMETTP 57
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 62 EQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 108
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 58 SKQSNKNYMASSYLSLTARAWERHSSYSCQVTHG--HTVEKSLSR 102
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 4
LAC5 MUSSP
ID LAC5 MUSSP STANDARD; PRT; 105 AA.
AC P20765;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-5 chain C region.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88196070; PubMed=3129289;
RA Mami F., Cazenave P.A., Kindt T.J.;
RT "Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
RL EMBO J. 7:117-122 (1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M35582; AAA39152.1; -.
CC HSSP; P01843; IJNH.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003597; Ig cl.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00407; IGC1; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC KW Immunoglobulin C region; Immunoglobulin domain.
CC FT NON_TER 1
CC FT DOMAIN 6 100 Ig-like.
CC FT DISULFID 27 86
CC FT DISULFID 104 104 Interchain (with heavy chain).
CC SQ SEQUENCE 105 AA; 11674 MW; AAB417DF68471A17 CRC64;

Query Match 21.8%; Score 126.5; DB 1; Length 105;
Best Local Similarity 30.6%; Pred. No. 0.0001;
Matches 33; Conservative 23; Mismatches 45; Indels 7; Gaps 3;

QY 3 PVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
Db 2 PKSDPLVTLFPLSLKNL-----QANKVTLVCLVSEFPYPTGLVVDWKVDGVPVVGQVETTP 57
QY 62 EEQYNSTYRVSVLTVLHVDWLNKGYCKVSNKGLPSSIEKTSKAK 109
Db 58 SKQTNNKYWSSVLTLSIQWMPHSRVSCTVTHEG--NTVEKSVSPAE 103

RESULT 5
LACS_MOUSE STANDARD; PRT; 105 AA.
AC P20764;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-5 chain C region.
GN Name=Igl-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87065143; PubMed=3024017;
RA Sakaguchi N., Melchers F.;
RT "Lambda 5, a new light-chain-related locus selectively expressed in pre-B lymphocytes.";
RL Nature 324:579-582 (1986).
CC -1- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; M30387; -; NOT_ANNOTATED_CDS.
CC DR HSSP; P01843; IJNH.
CC DR MGD; MGI:96529; Igl-5.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003597; Ig cl.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR SMART; SM00407; IGC1; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC DR PROSITE; PS00290; IG_MHC; FALSE NEG.
CC KW Immunoglobulin C region; Immunoglobulin domain.
CC FT NON_TER 1

FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11678 MW; 1F210915904A86A5 CRC64;

Query Match 21.1%; Score 122.5; DB 1; Length 105;
Best Local Similarity 31.5%; Pred. No. 0.00026;
Matches 34; Conservative 25; Mismatches 42; Indels 7; Gaps 5;

QY 3 PVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
Db 2 PKSDPLVTLFPLSLKNL-----QANKVTLVCLVSE--FYPGTLVVDWKVDGVPVVGQVETTP 57
QY 62 EEQYNSTYRVSVLTVLHVDWLNKGYCKVSNKGLPSSIEKTSKAK 109
Db 58 SKQTNNKYWSSVLTLSIQWMPHSRVSCTVTHEG--NTVEKSVSPAE 103

RESULT 6
Q8TCJ5 PRELIMINARY; PRT; 106 AA.
AC Q8TCJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp667J0810;
GN Name=DKFZp667J0810;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR HSSP; P01842; ILIL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 20.9%; Score 121.5; DB 2; Length 106;
Best Local Similarity 29.5%; Pred. No. 0.00033;
Matches 31; Conservative 22; Mismatches 45; Indels 7; Gaps 4;

QY 3 PVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
Db 3 PKAASVTLFPSSSE--LQANKATLVCLISD--FYPGAVTVAWKADSSPVKAGVETTP 58
QY 62 EEQYNSTYRVSVLTVLHVDWLNKGYCKVSNKGLPSSIEKTS 106
Db 59 SKQSNKYAASSVLTLPQWKSYSQCVTHEG--STVEKTA 101

RESULT 7
LAC_HUMAN STANDARD; PRT; 105 AA.
AC P01842; P80423;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda chain C regions.
GN Name=IGLC1;
```



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FT HELIX 15 19
FT TURN 20 21
FT STRAND 24 32
FT STRAND 38 43
FT TURN 44 45
FT STRAND 46 48
FT STRAND 52 59
FT TURN 61 62
FT STRAND 65 72
FT HELIX 75 80
FT STRAND 84 89
FT STRAND 94 99
SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;

Query Match 20.4%; Score 118.5; DB 1; Length 105;
Best Local Similarity 28.6%; Pred. No. 0.00064;
Matches 30; Conservative 23; Mismatches 45; Indels 7; Gaps 4;

QY 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61
DB 2 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYPGAVTVAMKADSSPVKAGVETTTP 57

QY 62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIK 106
DB 58 SKQSNKNKYAASSFLHLTANQWKSYQSVTCQVTHEG--HTVEKSLAPAE 103

RESULT 8
LAC_RABIT STANDARD; PRT; 105 AA.
AC P01847;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-FEB-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE
RX MEDLINE=82091105; PubMed=6797414;
RA Garcia I., Jaton J.-C.;
RT "The primary structure of the constant region of Basilea-rabbit
RT immunoglobulin lambda-chains.";
RL Biochem. J. 197; 177-183 (1981).
CC -I- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
CC specificity.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02130; L7RB.
DR HSSP; P01842; 1AQQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 19.5%; Score 113.5; DB 1; Length 105;
Best Local Similarity 27.8%; Pred. No. 0.002;
Matches 30; Conservative 21; Mismatches 50; Indels 7; Gaps 4;

QY 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
DB 2 PAVTPSVILFPPSSEE--LQDNKATLVCLISDIPR--TVKNWVKADGNSVTGGVDTPQ 57
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QY 62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIK 109
DB 58 SKQSNKNKYAASSFLHLTANQWKSYQSVTCQVTHEG--HTVEKSLAPAE 103

RESULT 9
KAC4_RABIT STANDARD; PRT; 103 AA.
AC P01840;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa-b4 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83300036; PubMed=6412231;
RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
RT allotype J-C locus and evidence for several b4-related sequences in
RT the rabbit genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713 (1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a
RT kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806 (1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.S., Kindt T.J., Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody
RT to streptococcal carbohydrate. II. Sequence determination of peptides
RT from tryptic and peptic digests.";
RL J. Biol. Chem. 250:3289-3296 (1975).
CC -I- MISCELLANEOUS: This chain was obtained from antibody to the
CC specific carbohydrate of group C Streptococci and was isolated
CC from the serum of a single rabbit.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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DR EMBL; X00231; CAA25051.1; -.
DR PIR; A93971; K4RB.
DR HSSP; P01837; 1KCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 5 95 Ig-like.
FT DISULFID 26 85
FT DISULFID 103 103 Interchain (with a heavy chain).
FT CONFLICT 58 58 N -> D (in Ref. 3).
SQ SEQUENCE 103 AA; 11043 MW; 5FC5ACC8B60E68DB CRC64;

Query Match 19.4%; Score 112.5; DB 1; Length 103;
Best Local Similarity 31.7%; Pred. No. 0.0024;
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Matches 33; Conservative 19; Mismatches 39; Indels 13; Gaps 6;
Qy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE-----VHNAKT 58
Db 2 PVA-PTVLIFPPAADQ--VATGTVIVCV---ANKYFPDVTVTWEVDGTTTGTGIESKT 55
Qy 59 KPREEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIE 102
Db 56 P--QNSADCTYNLSSTLTSTQNSHKEYTKVT-QGTTSVWQ 96

RESULT 10
LAC_PIG
ID LAC_PIG STANDARD; PRT; 105 AA.
AC P01846;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
PP SEQUENCE.
RX MEDLINE=7800254; PubMed=409425;
RA Novotny J., Franek F., Margolies M.N., Haber E.;
RT "Amino acid sequence of normal (microheterogeneous) porcine
immunoglobulin lambda chains.";
RL Biochemistry 16:3765-3772(1977).
CC -1- MISCELLANEOUS: This chain was obtained from a mixture of normal
immunoglobulins.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02129; L1PG.
DR HSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 2 100 Ig-like.
FT DISULFID 27 86 Interchain (with heavy chain).
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11003 MW; 3817AABD747C396 CRC64;

Query Match 18.7%; Score 108.5; DB 1; Length 105;
Best Local Similarity 28.4%; Pred. No. 0.0061;
Matches 31; Conservative 20; Mismatches 49; Indels 9; Gaps 4;
Qy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA--KTKP 60
Db 2 PKAAPTNLFPSPSEEL----GTNKATLVCLISDFYPCGAVTVTWKAGGTTVQGVETKTP 57
Qy 61 REEQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109
Db 58 -SKQSNKYAASSYLALSADWKSSTGTCQVTHEG--TIVEKTVTPSE 103

RESULT 11
LAC1_RAT
ID LAC1_RAT STANDARD; PRT; 104 AA.
AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; M22520; AAA41419.1; ALT_INIT.
DR HSP; P01843; 1JNH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85 Interchain (with heavy chain).
FT DISULFID 103 103
SQ SEQUENCE 104 AA; 11565 MW; CBF71811F4BC878A CRC64;

Query Match 18.6%; Score 108; DB 1; Length 104;
Best Local Similarity 25.2%; Pred. No. 0.0068;
Matches 27; Conservative 23; Mismatches 51; Indels 6; Gaps 2;
Qy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
Db 2 PKATPSVTLFPSPSEEL---KTDKATLVCMVDFYPGVMTVMKADGTPITQGVETTP 57
Qy 63 EQNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 109
Db 58 FKQNNKYMATSYLLLTAKAWETHSNYSQVTHE--ENTVEKSLRAE 102

RESULT 12
KAC_MOUSE
ID KAC_MOUSE STANDARD; PRT; 106 AA.
AC P01837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
PP SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
RN [2]
PP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
RN [3]
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CC -----
DR EMBL; X00032; -; NOT_ANNOTATED_CDS.
DR PIR; A01363; AAA31355.1; -.
DR HSP; P01837; KSRB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT DOMAIN 1 1 Ig-like.
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
FT CONFLICT 1 1 A -> VA (in Ref. 2)
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 17.9%; Score 104; DB 1; Length 104;
Best Local Similarity 26.7%; Pred. No. 0.017;
Matches 28; Conservative 24; Mismatches 41; Indels 12; Gaps 5;

Qy 7 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG-----VEVHNAKTKPRE 62
Db 5 PTVLIFPPSPAE--LATGTATVVCV---ANKYFPDGTVTWQVDGKPLTTGIETSKTPQNS 59

Qy 63 EQYNSTYRVVSVLTVHLQDMLNGKYKCKVSNKGLPSSIEKTSK 107
Db 60 D--DCTYLSSTLTKSDEYNHSHDEYTCQVA-QGSGPVQVSFPR 101

RESULT 14
LAC2 RAT STANDARD; PRT; 104 AA.
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-2 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
RL and a single V lambda gene."
RL Gene 55:75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; M22521; AAA41420.1; ALT_INIT.
CC HSP; P01842; 2MCG.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00407; Igc1; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1

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FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85
FT DISULFID 103 103 Interchain (with heavy chain).
SQ SEQUENCE 104 AA; 11318 MW; F087906DE43F7276 CRC64;

Query Match 17.0%; Score 99; DB 1; Length 104;
Best Local Similarity 21.5%; Pred. No. 0.052;
Matches 23; Conservative 28; Mismatches 50; Indels 6; Gaps 3;

Qy 3 PVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
Db 2 PKSTPTLTVPFPSTES--LQGNKATLVCLISDFYPSDVEVA--WKANGAPISQGVDTANP 57

Qy 63 EQYNSTYRVVSVLTVHLQDMLNGKYKCKVSNKGLPSSIEKTSKAK 109
Db 58 TKQGNKYIASSFLRLTAEQWRSRNSFTQVTHEG--NTVEKSLSPAE 102

RESULT 15
KACB RABIT STANDARD; PRT; 106 AA.
AC P01839;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa-b4 chain C region.
GN Names=K-BAS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Basilea;
RX PubMed=11894960;
RA Heidmann O., Rougeon F.;
RT "Multiplicity of constant kappa light chain genes in the rabbit
RL genome: a b4b4 homozygous rabbit contains a kappa-bas gene."
RL EMBO J. 2:437-441(1983).
CC -1- MISCELLANEOUS: In Basilea rabbits, the major type of light chain
CC is lambda. The kappa chain shown is a minor component. All other
CC rabbit B allotypes have Cys-64.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; V01241; CAA24558.1; -.
CC ENBL; V00885; -; NOT_ANNOTATED_CDS.
CC PIR; A02121; K4RBBS.
CC HSP; P01837; 25C8.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 87
FT DISULFID 106 106 Interchain (with a heavy chain).
SQ SEQUENCE 106 AA; 11279 MW; AF9B928DDA853849 CRC64;

Query Match 17.0%; Score 99; DB 1; Length 106;
Best Local Similarity 29.4%; Pred. No. 0.053;
Matches 32; Conservative 21; Mismatches 44; Indels 12; Gaps 6;

Qy 3 PVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE-----VHNAKT 58

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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.3927 Seconds  
(without alignments)  
347.833 Million cell updates/sec

Title: US-09-674-857-1  
Perfect score: 581  
Sequence: 1 APPVAGPSVFLPPKPKDTL.....CKVSNKGLPSSIEKTSKAK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0  
Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep: \*  
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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	95.4	109	3	US-08-444-644-30
2	554	95.4	109	3	US-08-232-246A-30
3	542	93.3	110	3	US-08-444-644-21
4	542	93.3	110	3	US-08-232-246A-21
5	541	93.1	105	2	US-08-232-539D-60
6	540	92.9	109	2	US-08-070-116A-4
7	540	92.9	109	4	US-08-557-050-4
8	540	92.9	110	3	US-08-444-644-44
9	540	92.9	110	3	US-08-232-246A-44
10	518	89.2	110	3	US-08-444-644-38
11	518	89.2	110	3	US-08-232-246A-38
12	329	56.6	66	3	US-08-569-147-85
13	175	30.1	107	4	US-09-281-7608-36
14	166.5	28.7	106	2	US-08-232-539D-54
15	152	26.2	109	3	US-08-466-163B-1
16	152	26.2	109	4	US-09-802-096-1
17	152	26.2	109	4	US-09-802-077-1
18	141	24.3	100	1	US-08-422-101-10
19	141	24.3	100	1	US-08-422-091-10
20	141	24.3	100	2	US-08-422-092-10
21	141	24.3	100	2	US-08-788-800-7
22	141	24.3	100	3	US-08-422-093-10
23	141	24.3	100	3	US-08-422-112-10
24	139	23.9	105	3	US-09-025-769B-166
25	139	23.9	105	4	US-09-490-070A-166
26	139	23.9	105	4	US-09-490-153-166
27	139	23.9	105	4	US-09-490-324-166

28 139 23.9 106 2 US-08-378-939-40 Sequence 40, Appl  
29 139 23.9 106 2 US-08-761-277A-49 Sequence 49, Appl  
30 139 23.9 106 3 US-08-444-644-26 Sequence 26, Appl  
31 139 23.9 106 3 US-08-232-246A-26 Sequence 26, Appl  
32 139 23.9 107 1 US-08-422-101-8 Sequence 8, Appl  
33 139 23.9 107 1 US-08-422-091-8 Sequence 8, Appl  
34 139 23.9 107 2 US-08-422-092-8 Sequence 5, Appl  
35 139 23.9 107 2 US-08-788-800-5 Sequence 5, Appl  
36 139 23.9 107 3 US-08-422-093-8 Sequence 8, Appl  
37 139 23.9 107 3 US-08-422-112-8 Sequence 8, Appl  
38 139 23.9 107 4 US-09-301-593-20 Sequence 20, Appl  
39 139 23.9 108 4 US-09-313-942-13 Sequence 13, Appl  
40 135 23.2 106 2 US-08-378-939-42 Sequence 42, Appl  
41 133.5 23.0 109 2 US-08-646-981-6 Sequence 6, Appl  
42 130 22.4 109 1 US-08-436-463-8 Sequence 8, Appl  
43 130 22.4 109 1 US-08-024-253-8 Sequence 8, Appl  
44 129 22.2 106 1 US-08-399-106A-7 Sequence 7, Appl  
45 129 22.2 106 1 US-08-433-105A-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-444-644-30  
; Sequence 30, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Fiden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-444-644-30

Query Match 95.4%; Score 554; DB 3; Length 109;  
Best Local Similarity 93.6%; Pred. No. 2.4e-56;  
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
Db 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109  
Db 61 REQQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109

RESULT 2

US-08-232-246A-30  
; Sequence 30, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,246A  
; FILING DATE: 04-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-232-246A-30

Query Match 95.4%; Score 554; DB 3; Length 109;  
Best Local Similarity 93.6%; Pred. No. 2.4e-56;  
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

Db 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109  
Db 61 REQQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109

RESULT 3

US-08-444-644-21  
; Sequence 21, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-444-644-21

Query Match 93.3%; Score 542; DB 3; Length 110;  
Best Local Similarity 95.3%; Pred. No. 5.9e-55;  
Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 63  
Db 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 64  
QY 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109  
Db 65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

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RESULT 4
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Eriden, Phillip M.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-21

Query Match 93.3%; Score 542; DB 3; Length 110;
Best Local Similarity 95.3%; Pred. No. 5.9e-55;
Matches 101; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
;
Db 5 LGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
;
Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 110
;

RESULT 5
US-08-232-539D-60
; Sequence 60, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.

```

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; TITLE OF INVENTION: IgE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-232-539D-60

Query Match 93.1%; Score 541; DB 2; Length 105;
Best Local Similarity 97.1%; Pred. No. 7.2e-55;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
;
Db 1 GPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 60
;
Qy 66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 61 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETIKAK 104
;

RESULT 6
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/070,116A
/ FILING DATE: 01-JUN-1993
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: ARCD:082
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 109 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-070-116A-4

Query Match          92.9%; Score 540; DB 2; Length 109;
Best Local Similarity 95.3%; Pred. No. 9.9e-55;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db  4 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63

QY  64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db  64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 7
US-08-557-050-4
/ Sequence 4, Application US/08557050
/ Patent No. 6491916
/ GENERAL INFORMATION:
/ APPLICANT: Bluestone, Jeffrey A.
/ APPLICANT: Zivin, Robert A.
/ APPLICANT: Jolliffe, Linda K.
/ TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
/ TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
/ TITLE OF INVENTION: ANTIBODIES
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/557,050
/ FILING DATE: Concurrently Herewith
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/06198
/ FILING DATE: 01-JUN-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/070,116
/ FILING DATE: 01-JUN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: ARCD:208
/ TELECOMMUNICATION INFORMATION:
```

```
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 109 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-557-050-4

Query Match          92.9%; Score 540; DB 4; Length 109;
Best Local Similarity 95.3%; Pred. No. 9.9e-55;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db  4 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63

QY  64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db  64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 8
US-08-444-644-44
/ Sequence 44, Application US/08444644
/ Patent No. 6015555
/ GENERAL INFORMATION:
/ APPLICANT: Friden, Phillip M.
/ TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
/ TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
/ TITLE OF INVENTION: CONJUGATES
/ NUMBER OF SEQUENCES: 46
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
/ STREET: Two Militia Drive
/ CITY: Lexington
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02173
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/444,644
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/232,246
/ FILING DATE: 07-JUL-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/800,458
/ FILING DATE: 26-NOV-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US90/05077
/ FILING DATE: 07-SEP-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/404,089
/ FILING DATE: 07-SEP-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wagner, Richard W.
/ REGISTRATION NUMBER: 34,480
/ REFERENCE/DOCKET NUMBER: ALX88-15AAA2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 861-6240
/ TELEFAX: (617) 861-9540
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 110 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
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```
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-44

Query Match      92.9%; Score 540; DB 3; Length 110;
Best Local Similarity 95.3%; Pred. No. 1e-54; 2; Indels 0; Gaps 0;
Matches 101; Conservative 3; Mismatches 3;

Qy 4 VAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
;
Db 5 LGGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
;
Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
;

RESULT 9
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTI-BODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-44

Query Match      92.9%; Score 540; DB 3; Length 110;
Best Local Similarity 95.3%; Pred. No. 1e-54; 2; Indels 0; Gaps 0;
Matches 101; Conservative 3; Mismatches 3;

Qy 4 VAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
;
Db 5 LGGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
;
Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
;

RESULT 10
US-08-444-644-38
; Sequence 38, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTI-BODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-38

Query Match      89.2%; Score 518; DB 3; Length 110;
Best Local Similarity 91.5%; Pred. No. 3.5e-52;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
;
Db 5 LGGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
;
Qy 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
;
Db 65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
;
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```
RESULT 11
US-08-232-246A-38
; Sequence 36, Application US/082322246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-38

Query Match      89.2%; Score 518; DB 3; Length 110;
Best Local Similarity 91.5%; Pred. No. 3.5e-52;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNYVDGVEVHNAKTKPREE 63
      : |||||
Db      5 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKLREE 64

QY      64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 109
      : |||||
Db      65 QYNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKSAK 110

RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
```

```
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377rie, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-85

Query Match      56.6%; Score 329; DB 3; Length 66;
Best Local Similarity 96.8%; Pred. No. 1.2e-30;
Matches 60; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKENYVDGVEVHNAKTKPREE 63
      : |||||
Db      5 LGGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVFNWYVDGVEVHNAKTKPREE 64

QY      64 QY 65
      : ||
Db      65 QY 66

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (413)..(414) stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (451)..(451)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (460)..(462)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (500)..(500)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (530)..(530)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (568)..(568)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (847)..(849)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (853)..(853)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1382)..(1382)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1832)..(1832)  
OTHER INFORMATION: "n" stands for any nucleic acid

US-09-281-760E-36

Query Match 30.18; Score 175; DB 4; Length 107;  
Best Local Similarity 35.08; Pred. No. 1.3e-12;  
Matches 36; Conservative 23; Mismatches 42; Indels 2; Gaps 2;  
QY 6 GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65  
DB 5 GVSLSLPPSPFLD-LYVHKAPKITCLVVDLATWE-GNNLTWYRESKEPVPNPVPLNKDHF 62  
QY 66 NSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 108  
DB 63 NGTITVTSLPVTNDWIEGETYTCRVTHPHLPKDIVRSIAKA 105

RESULT 14  
US-08-232-539D-54  
Sequence 54, Application US/08232539D  
Patent No. 5965709  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Ige Antagonists  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/178583  
FILING DATE: 07-JAN-1994  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-54

Query Match 28.7%; Score 166.5; DB 2; Length 106;  
Best Local Similarity 34.3%; Pred. No. 1.3e-11;  
Matches 35; Conservative 22; Mismatches 44; Indels 1; Gaps 1;  
QY 6 GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65  
DB 1 GVSAYLSRSPFPD-LFIRKSPITICLVVDLAPSGKGTVNLTSRASGKPVNHSRKEKQR 59  
QY 66 NSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 107  
DB 60 NGTLTSTLPLVGTDRDIEGETYTCRVTHPHLPALMRSTTK 101

RESULT 15  
US-08-466-163B-1  
Sequence 1, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 1  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-466-163B-1

Query Match 26.2%; Score 152; DB 3; Length 109;  
Best Local Similarity 34.3%; Pred. No. 6.2e-10;  
Matches 35; Conservative 21; Mismatches 44; Indels 2; Gaps 2;  
QY 6 GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65  
DB 6 GVSAYLSRSPFPD-LFIRKSPITICLVVDLAPSGKGTVNLTSRASGKPVNHSRKEKQR 64  
QY 66 NSTYRVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIK 107

Db 65 NGTLTVTSTLPVGTDRDWIEG-ETQCRVTHPHLPRALMRSTTK 105  
Search completed: November 17, 2005, 07:53:55  
Job time : 24.3927 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 17, 2005, 07:47:15 ; Search time 82.3721 Seconds  
(without alignments)  
553.666 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTIKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 892101

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	98.6	109	18	US-10-959-318-11
2	573	98.6	109	18	US-10-959-318-12
3	562.5	96.8	110	18	US-10-959-318-9
4	562.5	96.8	110	18	US-10-959-318-10
5	559	96.2	109	18	US-10-959-318-15
6	559	96.2	109	18	US-10-959-318-16
7	554	95.4	109	18	US-10-959-318-2
8	548.5	94.4	110	18	US-10-959-318-13
9	548.5	94.4	110	18	US-10-959-318-14
10	548	94.3	110	18	US-10-959-318-7
11	548	94.3	110	18	US-10-959-318-8

12	547	94.1	109	18	US-10-627-556-270	Sequence 270, App
13	546	94.0	109	18	US-10-959-318-17	Sequence 17, Appl
14	546	94.0	109	18	US-10-959-318-18	Sequence 18, Appl
15	544.5	93.7	110	20	US-11-018-102-23	Sequence 23, Appl
16	542.5	93.4	110	20	US-11-018-102-25	Sequence 25, Appl
17	542	93.3	109	14	US-10-207-655-220	Sequence 220, App
18	542	93.3	109	18	US-10-627-556-14	Sequence 14, Appl
19	542	93.3	110	15	US-10-370-749-23	Sequence 23, Appl
20	542	93.3	110	18	US-10-959-318-1	Sequence 1, Appl
21	542	93.3	110	20	US-11-018-102-22	Sequence 22, Appl
22	540	92.9	109	14	US-10-267-286A-4	Sequence 4, Appl
23	540	92.9	110	18	US-10-959-318-4	Sequence 4, Appl
24	540	92.9	110	18	US-10-959-318-21	Sequence 21, Appl
25	540	92.9	110	20	US-11-018-102-24	Sequence 24, Appl
26	538	92.6	109	18	US-10-627-556-294	Sequence 294, App
27	537	92.4	109	14	US-10-020-354-80	Sequence 80, Appl
28	537	92.4	109	18	US-10-627-556-258	Sequence 258, App
29	537	92.4	109	18	US-10-627-556-278	Sequence 278, App
30	537	92.4	109	18	US-10-627-556-302	Sequence 302, App
31	537	92.4	110	15	US-10-370-749-53	Sequence 53, Appl
32	535	92.1	110	15	US-10-370-749-51	Sequence 51, Appl
33	535	92.1	110	18	US-10-959-318-22	Sequence 22, Appl
34	534	91.9	109	14	US-10-207-655-322	Sequence 322, App
35	534	91.9	109	18	US-10-627-556-92	Sequence 92, Appl
36	534	91.9	110	18	US-10-959-318-5	Sequence 5, Appl
37	534	91.9	110	18	US-10-959-318-6	Sequence 6, Appl
38	534	91.9	110	18	US-10-959-318-25	Sequence 25, Appl
39	533	91.7	110	18	US-10-959-318-23	Sequence 23, Appl
40	533	91.7	110	18	US-10-959-318-24	Sequence 24, Appl
41	532	91.6	110	17	US-10-491-653-22	Sequence 22, Appl
42	528	90.9	102	18	US-10-609-783B-54	Sequence 54, Appl
43	526	90.5	102	18	US-10-609-783B-57	Sequence 57, Appl
44	526	90.5	102	18	US-10-609-783B-59	Sequence 59, Appl
45	524	90.2	110	18	US-10-959-318-3	Sequence 3, Appl

## ALIGNMENTS

## RESULT 1

US-10-959-318-11  
; Sequence 11, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; APPLICANT: Clark, Michael R  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 11  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)  
; OTHER INFORMATION: mutations  
US-10-959-318-11

Query Match 98.6%; Score 573; DB 18; Length 109;

Best Local Similarity 99.1%; Pred. No. 1.9e-48; Mismatches 1; Indels 0; Gaps 0;  
Matches 108; Conservative

Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

Db 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

[illegible]

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RESULT 2
US-10-959-318-12
; Sequence 12, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a,
; OTHER INFORMATION: mutations
US-10-959-318-12

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Query Match	98.6%	Score 573;	DB 18;	Length 109;
Best Local Similarity	99.1%;	Pred. No. 1.9e-48;		
Matches 108;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

[illegible]

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RESULT 3
US-10-959-318-9
; Sequence 9, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a,
US-10-959-318-9

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Query Match	96.8%	Score 562.5	DB 18	Length 110
Best Local Similarity	98.2%	Pred. No. 2e-47		
Matches 108	Conservative	0	Mismatches 1	Gaps 1
			Indels	1

Qy	1	APPA-GRPVFLPPPKD	TLMI	STPEVTCVVVDVSHEDPEVK	NWYVDGVEVHNATK	59
Db	1	APPAVGSPVFLPPPKD	TLMI	STPEVTCVVVDVSDPEVK	NWYVDGVEVHNATK	60
Qy	60	PREEQYNSTYRVVSVLT	VLVH	QDLNGLGKEYCKVSNKGLPSS	IEKTI	109
Db	61	PREEQYNSTYRVVSVLT	VLVH	QDLNGLGKEYCKVSNKGLPSS	IEKTI	110

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RESULT 4
US-10-959-318-10
US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a,
; OTHER INFORMATION: mutations
US-10-959-318-10

```

Query Match	96.8%	Score 562.5	DB 18	Length 110
Best Local Similarity	98.2%	Pred. No. 26-47		
Matches 108	Conservative	0	Mismatches 1	Indels 11
			Gaps 1	

	Qy	Qy	Db	Qy	Db
1	APVIA-GRSVFLPPKPKD	TLMI	STP	PTV	CVVVDVSHDDPEVKFN
59					VYDGVGVHNAKTK
1	APVAGG	SVFLPPKPKD	TLMI	STP	PTV
60					CVVVDVSEEDPEVKFN
109					VYDGVGVHNAKTK
60	PREEQNSTYR	VVSVLT	LH	QD	WLN
109					QKYSNKG
110					LPSSIEK
61	PREEQNSTYR	VVSVLT	LH	QD	WLN
110					QKYSNKG
111					LPSSIEK

```

RESULT 5
US-10-959-318-15
; Sequence 15, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: ARMOUR, Kathryn L
; APPLICANT: CLARK, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b
; OTHER INFORMATION: mutations

```

```

US-10-959-318-15
Query Match      96.2%; Score 559; DB 18; Length 109;
Best Local Similarity 96.3%; Pred. No. 4.4e-47;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 109

RESULT 6
US-10-959-318-16
; Sequence 16, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and e (E268)
US-10-959-318-16

Query Match      96.2%; Score 559; DB 18; Length 109;
Best Local Similarity 96.3%; Pred. No. 4.4e-47;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSEDEPEVKFNWYVDGVEVHNAKTKP 60
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 109

RESULT 7
US-10-959-318-2
; Sequence 2, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-318-2

Query Match      95.4%; Score 554; DB 18; Length 109;
Best Local Similarity 93.6%; Pred. No. 1.4e-46;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Qy 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 109

RESULT 8
US-10-959-318-13
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
US-10-959-318-13

Query Match      94.4%; Score 548.5; DB 18; Length 110;
Best Local Similarity 95.5%; Pred. No. 4.8e-46;
Matches 105; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 APPVA-GPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
Db 1 APPVAGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSDPEVKFNWYVDGVEVHNAKTK 60
Qy 60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 9
US-10-959-318-14
; Sequence 14, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
US-10-959-318-14

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; SEQ ID NO 14
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268)
US-10-959-318-14

Query Match          94.4%; Score 548.5; DB 18; Length 110;
Best Local Similarity 95.5%; Pred. No. 4.8e-46;
Matches 105; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
Db 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60

QY 60 PREEQNSTYRVVSVLTVTLHODWLNKGKCKVSNKGLPSSIEKTIISKAK 109
Db 61 PREEQNSTYRVVSVLTVTLHODWLNKGKCKVSNKALPAPIEKTIISKAK 110

RESULT 10
US-10-959-318-7
; Sequence 7, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)
US-10-959-318-7

Query Match          94.3%; Score 548; DB 18; Length 110;
Best Local Similarity 97.2%; Pred. No. 5.3e-46;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKPREE 64

QY 64 QYNSTYRVVSVLTVTLHODWLNKGKCKVSNKGLPSSIEKTIISKAK 109
Db 65 QYNSTYRVVSVLTVTLHODWLNKGKCKVSNKGLPSSIEKTIISKAK 110

RESULT 11
US-10-959-318-8
; Sequence 8, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
```

```

; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and e (E268)
US-10-959-318-8

Query Match          94.3%; Score 548; DB 18; Length 110;
Best Local Similarity 97.2%; Pred. No. 5.3e-46;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKPREE 64

QY 64 QYNSTYRVVSVLTVTLHODWLNKGKCKVSNKGLPSSIEKTIISKAK 109
Db 65 QYNSTYRVVSVLTVTLHODWLNKGKCKVSNKGLPSSIEKTIISKAK 110

RESULT 12
US-10-627-556-270
; Sequence 270, Application US/10627556
; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 270
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-10-627-556-270

Query Match          94.1%; Score 547; DB 18; Length 109;
Best Local Similarity 96.2%; Pred. No. 6.6e-46;
Matches 102; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 4 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63

QY 64 QYNSTYRVVSVLTVTLHODWLNKGKCKVSNKGLPSSIEKTIISKAK 109
Db 64 QYNSTYRVVSVLTVTLHODWLNKGKCKVSNKALPASIEKTIISKAK 109

RESULT 13
US-10-959-318-17
```

```

; Sequence 17, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta d (D268) mutation
US-10-959-318-17

Query Match          94.0%; Score 546; DB 18; Length 109;
Best Local Similarity 92.7%; Pred. No. 8.3e-46;
Matches 101; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
    |||||
Db 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
    |||||

Qy 61 REEQYNSTYRVSVLTVLVHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 109
    |||||
Db 61 REEQFNSTFRVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKTK 109
    |||||

RESULT 14
US-10-959-318-18
; Sequence 18, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta e (E268) mutation
US-10-959-318-18

Query Match          94.0%; Score 546; DB 18; Length 109;
Best Local Similarity 92.7%; Pred. No. 8.3e-46;
Matches 101; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
    |||||
Db 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSEEDPEVQFNWYVDGVEVHNAKTKP 60
    |||||

Qy 61 REEQYNSTYRVSVLTVLVHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 109
    |||||
Db 61 REEQFNSTFRVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKTK 109
    |||||
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RESULT 15
US-11-018-102-23
; Sequence 23, Application US/11018102
; Publication No. US20050136061A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5045 USA NP
; CURRENT APPLICATION NUMBER: US/11/018,102
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: engineered G1 CH2
US-11-018-102-23

Query Match          93.7%; Score 544.5; DB 20; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.2e-45;
Matches 104; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 APPVA-GPSVFLPPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
    |||||
Db 1 APEAAGGPSVFLPPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
    |||||

Qy 60 FREEQYNSTYRVSVSVLTVLVHODWLNKGEYKCKVSNKGLPSSIEKTIISKAK 109
    |||||
Db 61 FREEQYNSTYRVSVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKAK 110
    |||||

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Job time : 82.3721 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 90.8333 Seconds  
(without alignments)  
464.112 Million cell updates/sec

Title: US-09-674-857-2  
Perfect score: 580  
Sequence: 1 APPVAGPSVFLPPKPKDTL.....CKVSNKGLPSSIEKTSKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	100.0	326	8	ADF77155
2	580	100.0	447	8	ADQ17121
3	580	100.0	462	8	ADF77154
4	577	99.5	436	7	ADM33853
5	577	99.5	436	8	ADR48984
6	577	99.5	448	7	ADM33376
7	572	98.6	109	2	AAR41709
8	572	98.6	109	3	RAY54997
9	572	98.6	217	3	AAB07476
10	572	98.6	217	4	AAB76423
11	572	98.6	217	4	AAB67203
12	572	98.6	217	5	ABG78434
13	572	98.6	217	6	ABR42440
14	572	98.6	217	8	ADH75378
15	572	98.6	228	5	ABG31095
16	572	98.6	228	8	ADR48993
17	572	98.6	310	8	ADR84436
18	572	98.6	310	8	ADR68578
19	572	98.6	326	4	AAE02643
20	572	98.6	326	5	RAM47857
21	572	98.6	326	5	ABG30462
22	572	98.6	326	5	ABG77148
23	572	98.6	326	6	AAE32916
24	572	98.6	326	6	AAE32628
25	572	98.6	326	6	AAO30894

26	572	98.6	326	7	ADQ97353	Adq97353 Human IgG
27	572	98.6	326	7	ADF75002	Adf75002 Human Ig
28	572	98.6	326	8	ADM41541	Adm41541 Anti-inte
29	572	98.6	326	8	ADQ95469	Adq95469 Human IgG
30	572	98.6	326	8	ADR28562	Adr28562 Human ant
31	572	98.6	381	2	AAO6895	Aao6895 Human IL-
32	572	98.6	432	2	AAR26782	Aar26782 CD4-gamma
33	572	98.6	432	2	AAR46678	Aar46678 CD4-gamma
34	572	98.6	432	3	AAO85079	Aao85079 Human CD4
35	572	98.6	432	4	AAB67322	Aab67322 CD4-gamma
36	572	98.6	432	4	AAB80883	Aab80883 Human CD4
37	572	98.6	432	6	ABG71122	Abg71122 CD4-gamma
38	572	98.6	442	4	AAB72230	Aab72230 Humanised
39	572	98.6	443	2	AAO31670	Aao31670 Human IgG
40	572	98.6	445	8	ADK52332	Adk52332 Human ant
41	572	98.6	445	8	ADK52384	Adk52384 Human ant
42	572	98.6	445	8	ADK52296	Adk52296 Human ant
43	572	98.6	445	8	ADK52312	Adk52312 Human ant
44	572	98.6	446	7	ADM18320	Adm18320 Human CD4
45	572	98.6	451	3	AAO93734	Aao93734 The heavy

ALIGNMENTS

RESULT 1  
ADF77155  
ID ADF77155 standard; protein; 326 AA.  
XX  
AC ADF77155;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Anti-VAP-1 monoclonal antibody H chain constant region.  
XX  
KW complementarity determining region; CDR; mouse;  
KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;  
KW chimeric; inflammatory disorder; rheumatoid arthritis;  
KW inflammatory bowel disease; autoimmune disease; psoriasis;  
KW immunoscintigraphic imaging.  
XX  
OS Homo sapiens.  
XX  
PN WO2003093319-A1.  
XX  
PD 13-NOV-2003.  
XX  
PF 28-APR-2003; 2003WO-FI000330.  
XX  
PR 29-APR-2002; 2002FI-00000807.  
XX  
PA (BIOT-) BIOTIE THERAPIES CORP.  
XX  
PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;  
XX  
WPI; 2004-022642/02.  
XX  
New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and encoding nucleic acid molecules, useful for diagnosing and treating chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.

Claim 18; SEQ ID NO 16; 56pp; English.

This sequence represents the constant region of a human anti-Vascular Adhesion Protein-1 (VAP-1) antibody heavy chain. This sequence may be used in the production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic acid molecules, polypeptides or antibodies are useful in treating VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis, inflammatory bowel disease, autoimmune diseases or psoriasis. The chimeric VAP-1 antibody is further used for in vitro and in vivo diagnostic applications, including in vivo immunoscintigraphic imaging of inflammation sites. The chimeric Mab's of the invention have improved kinetic properties compared to the corresponding murine antibodies.

```

XX SQ Sequence 326 AA;
Query Match 100.0%; Score 580; DB 8; Length 326;
Best Local Similarity 100.0%; Pred. No. 9e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 60
DB 111 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 170

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109
DB 171 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 219

RESULT 2
ADQ17121
ID ADQ17121 standard; protein; 447 AA.
XX AC ADQ17121;
XX DT 07-OCT-2004 (first entry)
XX Humanised anti-NGF antibody E3 heavy chain full-length protein.
XX nerve growth factor; anti-NGF antibody; E13.5 trigeminal neurone;
XX analgesic; immunomodulator; post-surgical pain; rheumatoid arthritis;
XX osteoarthritis; inflammatory cachexia; gene therapy;
XX monoclonal antibody 911; humanised antibody E3; heavy chain; murine;
XX mouse; mutant; mutein.
XX Mus sp.
XX Homo sapiens.
XX Synthetic.

XX FH Key Location/Qualifiers
XX Region 26..35
XX /note= "Extended CDR (complementarity determining region)
XX 1"
XX Misc-difference 34
XX /note= "Wild-type Ile of murine Mab 911 substituted by
XX Leu"
XX Region 50..65
XX /note= "Extended CDR (complementarity determining region)
XX 2"
XX Misc-difference 50
XX /note= "Wild-type Met of murine Mab 911 substituted by
XX Ile"
XX Misc-difference 63
XX /note= "Wild-type Leu of murine Mab 911 substituted by
XX Val"
XX Region 98..110
XX /note= "Extended CDR (complementarity determining region)
XX 3"
XX Misc-difference 101
XX /note= "Wild-type Tyr of murine Mab 911 substituted by
XX Trp"
XX Misc-difference 103
XX /note= "Wild-type Gly of murine Mab 911 substituted by
XX Ala"
XX WO2004058184-A2.
XX 15-JUL-2004.
XX 24-DEC-2003; 2003WO-US041252.
XX 24-DEC-2002; 2002US-0436905P.
XX 28-JAN-2003; 2003US-044322P.
XX 08-OCT-2003; 2003US-0510006P.
XX (RINA-) RINAT NEUROSCIENCE CORP.
PA

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XX PI Shelton DL, Pons J, Rosenthal A;
XX WPI; 2004-525786/50.
XX N-PSDB; ADQ17170.
XX New anti-nerve growth factor antibodies for preventing or treating pain,
XX including post-surgical pain, rheumatoid arthritis pain or osteoarthritis
XX pain, or for treating inflammatory cachexia associated with rheumatoid
XX arthritis.
XX Claim 25; SEQ ID NO 16; 186pp; English.
XX PS The invention relates to a novel anti-nerve growth factor (NGF) antibody
XX which binds NGF with a KD of less than about 2 nM and inhibits human NGF-
XX dependent survival of mouse E13.5 trigeminal neurones with an IC50 of
XX about 100 or 10 pM or less, where the IC50 is measured in the presence of
XX about 15 or 1.5 pM of human NGF. The antibody of the invention
XX demonstrates analgesic and immunomodulator activities and may be useful
XX for preventing and/or treating pain, including post-surgical pain and
XX pain associated with rheumatoid arthritis or osteoarthritis. The antibody
XX may be further utilised for treating inflammatory cachexia associated
XX with rheumatoid arthritis, as well as during gene therapy procedures. The
XX current sequence is that of the humanised anti-NGF antibody E3 heavy
XX chain full-length protein of the invention which was synthesised via
XX grafting CDRs (complementarity determining regions) from murine anti-NGF
XX Mab (monoclonal antibody) 911 onto human framework sequences and
XX subsequently mutating the CDRs to improve binding.
XX SQ Sequence 447 AA;
Query Match 100.0%; Score 580; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 60
DB 232 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKP 291

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109
DB 292 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 340

RESULT 3
ADF77154
ID ADF77154 standard; peptide; 462 AA.
XX AC ADF77154;
XX DT 26-FEB-2004 (first entry)
XX Chimeric Anti-VAP-1 monoclonal antibody H chain.
XX complementarity determining region; CDR; mouse;
XX Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
XX chimeric; inflammatory disorder; rheumatoid arthritis;
XX inflammatory bowel disease; autoimmune disease; psoriasis;
XX immunoscintigraphic imaging.
XX Chimeric.
XX Mus sp.
XX Homo sapiens.
XX WO2003093319-A1.
XX 13-NOV-2003.
XX 28-APR-2003; 2003WO-FI000330.
XX 29-APR-2002; 2002FI-00000807.
XX (BIOT-) BIOTIE THERAPIES CORP.
PA

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XX  Jalkanen S, Salmi M, Laukkanen M, Clark MR;
XX  WPI; 2004-022642/02.
XX  N-PSDB; ADF77144.
XX  New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
XX  encoding nucleic acid molecules, useful for diagnosing and treating
XX  chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
XX  Claim 9; SEQ ID NO 15; 56pp; English.
XX  This sequence represents a chimeric human-mouse anti-Vascular Adhesion
XX  protein-1 (VAP-1) antibody heavy chain. This sequence may be used in the
XX  production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic
XX  acid molecules, polypeptides or antibodies are useful in treating VAP-1
XX  mediated inflammatory disorders, such as rheumatoid arthritis,
XX  inflammatory bowel disease, autoimmune diseases or psoriasis. The
XX  chimeric VAP-1 antibody is further used for in vitro and in vivo
XX  diagnostic applications, including in vivo immunoscintigraphic imaging of
XX  inflammation sites. The chimeric MAB's of the invention have improved
XX  kinetic properties compared to the corresponding murine antibodies.
XX  Sequence 462 AA;
XX  Query Match 100.0%; Score 580; DB 8; Length 462;
XX  Best Local Similarity 100.0%; Pred. No. 1.4e-50;
XX  Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
XX  247 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 306
XX  61 REEQFNSTFRVSVLTIVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
XX  307 REEQFNSTFRVSVLTIVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 355
XX  RESULT 4
XX  ADM33853
XX  ID ADM33853 standard; protein; 436 AA.
XX  AC ADM33853;
XX  03-JUN-2004 (first entry)
XX  Human HuEPO-L-vFc gamma2 fusion protein.
XX  Erythropoietin; EPO; immunoglobulin; IgG;
XX  fragment crystallisation region; Fc; chronic anaemia; renal disease;
XX  cancer chemotherapy; rheumatoid arthritis; AIDS;
XX  myelodysplastic syndrome; (HuEPO)-L-vFc gamma2; human.
XX  Homo sapiens.
XX  Synthetic.
XX  Key Location/Qualifiers
XX  Peptide 1..27
XX  /note= "Signal peptide"
XX  Protein 28..192
XX  /note= "EPO"
XX  Peptide 193..208
XX  /note= "Linker"
XX  Protein 209..436
XX  /note= "IgG2 Fc"
XX  Misc-difference 390
XX  /note= "Wild-type Pro substituted by Ser"
XX  XX
XX  US2003082749-A1.
XX  PN
XX  01-MAY-2003.
XX  PD
XX  17-AUG-2001; 2001US-00932812.
XX  PF
XX  17-AUG-2001; 2001US-00932812.
XX  (SUNL/) SUN L K.
XX  (SUNB/) SUN B N C.
XX  (SUNC/) SUN C R Y.
XX  Sun LK, Sun BNC, Sun CRY;
XX  WPI; 2003-616080/58.
XX  New recombinant human erythropoietin-L-vFc fusion proteins, useful for
XX  treating patients with chronic anemia caused by renal failure, cancer
XX  chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
XX  infection.
XX  Claim 3; Fig 2A; 14pp; English.
XX  The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
XX  fusion protein comprising HuEPO, a peptide linker, and a human
XX  immunoglobulin G Fc (fragment crystallisation region) variant. Also
XX  included is a carbohydrate-derived cell line producing the human
XX  erythropoietin-L-vFc fusion protein cited above in its growth medium in
XX  excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
XX  -L-vFc fusion protein exhibits an enhanced in vitro biological activity
XX  of at least 2-fold relative to that of recombinant HuEPO on a molar
XX  basis. The flexible peptide linker containing about 20 or fewer amino
XX  acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
XX  contains amino acid mutations to attenuate effector functions. The human
XX  IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
XX  Pro331Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
XX  human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The
XX  recombinant human erythropoietin-L-vFc fusion proteins are useful for
XX  treating patients with chronic anaemia caused by renal failure, cancer
XX  chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
XX  infection, or myelodysplastic syndrome. The increased activity and
XX  prolonged presence of the human erythropoietin-L-vFc fusion protein in
XX  the serum, as compared to prior art, leads to lower dosages and less
XX  frequent injections. Less fluctuations of the drug in serum
XX  concentrations means improved safety and tolerability, and less frequent
XX  injections result in better patient compliance and quality of life. The
XX  present sequence represents the fusion protein HuEPO-L-vFc gamma2.
XX  Sequence 436 AA;
XX  Query Match 99.5%; Score 577; DB 7; Length 436;
XX  Best Local Similarity 99.1%; Pred. No. 2.6e-50;
XX  Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX  1 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
XX  221 APPVAGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 280
XX  61 REEQFNSTFRVSVLTIVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
XX  281 REEQFNSTFRVSVLTIVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 329
XX  RESULT 5
XX  ADR48984
XX  ID ADR48984 standard; protein; 436 AA.
XX  AC ADR48984;
XX  02-DEC-2004 (first entry)
XX  HuEPO-L-Fc fusion protein.
XX  antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;
XX  anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
XX  AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
XX  Homo sapiens.

```

OS Synthetic.  
PN US2004175824-A1.  
XX 09-SEP-2004.  
PD  
XX 21-JAN-2004; 2004US-00761593.  
XX 17-AUG-2001; 2001US-00932812.  
XX (SUNL/) SUN L K.  
PA (SUNB/) SUN B N C.  
PA (SUNC/) SUN C R Y.  
XX  
XX Sun LK, Sun BNC, Sun CRY;  
XX WPI: 2004-634851/61.  
DR N-PSDB; ADR48983.  
XX  
XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
PT (HuEPO), a peptide linker, and a human Igg Fc variant, useful for  
PT treating chronic anemia due to renal diseases, cancer chemotherapy, or  
PT rheumatoid arthritis.  
XX  
XX Claim 3; SEQ ID NO 18; 31pp; English.  
XX  
XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
CC (HuEPO), a peptide linker, and a human Igg Fc variant, is new.  
CC INDEPENDENT CLAIMS are also included for the following: a Chinese hamster  
CC ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in  
CC its growth medium in excess of 10  $\mu$ microg/9 per million cells in a 24 hour  
CC period; and a method for making a recombinant fusion protein comprising  
CC HuEPO, a flexible peptide linker, and a human Igg Fc variant. Preferred  
CC Protein: The peptide linker containing 20 or fewer amino acids is present  
CC between HuEPO and the human Igg Fc variant, and comprises two or more  
CC amino acids selected from glycine, serine, alanine, and threonine. The  
CC human Igg Fc variant comprises a hinge, CH2, and CH3 domains of human  
CC IgG2 with Pro31Ser mutation comprising 436 amino acids (SEQ ID NO. 18).  
CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with  
CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.  
CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1  
CC with Leu234Val, Leu235Ala, and Pro31Ser mutations comprising 435 amino  
CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro  
CC biological activity similar to or higher than that of rHuEPO on a molar  
CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line  
CC producing the HuEPO-L-vFc fusion protein in its growth medium in excess  
CC of 30  $\mu$ microg/9 per million cells in a 24 hour period. The human Igg Fc  
CC variant comprises a hinge, CH2, CH3 domains of human Igg selected from  
CC IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,  
CC the Igg Fc contains amino acid mutations to attenuate effector functions,  
CC a flexible peptide linker containing 20 or fewer amino acids is present  
CC between HuEPO and human Igg Fc variant, and the HuEPO-L-vFc fusion  
CC protein exhibits in vitro biological activity similar to or higher than  
CC that of rHuEPO on a molar basis. Preferred Method: Making a recombinant  
CC fusion protein comprising HuEPO, a flexible peptide linker, and a human  
CC Igg Fc variant comprises: Generating a CHO-derived cell line; growing the  
CC cell line where the recombinant protein is expressed in its growth medium  
CC in excess of 10  $\mu$ microg/9 per million cells in a 24 hour period; and  
CC purifying the expressed protein from (b), where the recombinant fusion  
CC protein exhibits in vitro biological activity similar to or higher than  
CC that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological  
CC data given. None given. Administration can be through subcutaneous or  
CC intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion  
CC protein is useful for treating patients with chronic anemia due to renal  
CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for  
CC HIV infection, or myelodysplastic syndrome. It is also useful in the  
CC treatment of renal failure. A fusion protein was assembled from several  
CC DNA segments. To obtain the gene encoding the leader peptide and mature  
CC protein of human erythropoietin (EPO), cDNA library of human fetal liver  
CC or kidney was used as the template in polymerase chain reaction (PCR).  
CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a  
CC restriction enzyme cleavage site is used as the 5' oligonucleotide  
CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon

CC and incorporates a BamHI site. The resulting DNA fragments of  
CC approximately 600 bp were inserted into a holding vector such as pUC19 at  
CC the HindIII and BamHI sites to give the pPEO plasmid. The sequence of the  
CC human EPO gene was confirmed by DNA sequencing.  
XX  
XX Sequence 436 AA;  
Query Match 99.5%; Score 577; DB 8; Length 436;  
Best Local Similarity 99.1%; Pred. No. 2.6e-50;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDSHEDPEVQFNWYVDGVEVHNATKP 60  
Db 221 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDSHEDPEVQFNWYVDGVEVHNATKP 280  
QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109  
Db 281 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 329  
RESULT 6  
ADM33376  
ID ADM33376 standard; protein; 448 AA.  
XX AC ADM33376;  
XX DT 03-JUN-2004 (first entry)  
XX DE Human GCSF-L-fragment of crystallisation gamma 2 fusion protein.  
XX cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy;  
KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;  
KW immunoglobulin G; Igg; fragment of crystallisation; immune disorder;  
KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;  
KW bone marrow transplantation; chronic neutropenia; fusion protein;  
KW fragment of crystallisation gamma 2; Fc gamma 2.  
XX Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Peptide 1..30 /label= GCSF leader peptide  
FT Protein 31..448 /note= "Mature human GCSF-L-fragment of crystallisation  
gamma 2 fusion"  
FT Misc-difference 331 /note= "Wild type Pro substituted by Ser"  
FT US2003082679-A1.  
XX 01-MAY-2003.  
XX 01-OCT-2001; 2001US-00968362.  
XX 01-OCT-2001; 2001US-00968362.  
XX (SUNL/) SUN L K.  
PA (SUNB/) SUN B N C.  
PA (SUNC/) SUN C R Y.  
XX Sun LK, Sun BNC, Sun CRY;  
XX WPI: 2003-585400/55.  
DR N-PSDB; ADM33375.  
XX  
XX New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-  
PT vFc fusion protein for treating immune or hematopoietic system disorders  
PT comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G  
PT Fc variant.  
XX  
XX Disclosure; Fig 2A; 15pp; English.  
PS  
XX



capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FcγRIIIb) causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding of a second binding molecule, e.g. an antibody, to the target molecule. The binding molecule is useful for the treatment of graft-vs-host disease, organ transplant rejection, bone-marrow transplant rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia and arthritis), autoimmunity (e.g. foetal/neonatal alloimmune thrombocytopenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HBN (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FcγRIIIb and desirable IgG properties have been retained. The polypeptides do not contain non-human amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FcRn (neonatal Fc receptor)

XX Sequence 109 AA;

Query Match 98.6%; Score 572; DB 3; Length 109;  
Best Local Similarity 99.1%; Pred. No. 1.6e-50;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60

Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60

QY 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

Db 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

RESULT 9

AAB07476

ID AAB07476 standard; protein; 217 AA.

XX AAB07476;

DT 20-OCT-2000 (first entry)

DE Amino acid sequence of native IgG Fc region humIgG2.

XX IgG antibody; light chain; Fc region; effector function; cancer; allergy;  
KW asthma; LFA-1-mediated disorder; tumour; cancer.

XX Homo sapiens.

PN WO200042072-A2.

XX 20-JUL-2000.

PF 14-JAN-2000; 2000WO-US000973.

XX 15-JAN-1999; 99US-0116023P.

XX (GETH ) GENENTECH INC.

XX Presta 1G;

XX WPI; 2000-476035/41.

XX New Fc region-containing polypeptides that have altered effector function  
PT due to one or more amino acid modifications in the Fc region, useful in  
PT the treatment of cancer and allergic conditions such as asthma.

PS Disclosure; Fig 22A; 132pp; English.

XX AAB07474-78 represent native IgG Fc regions. The proteins are used to  
CC produce Fc region-containing polypeptides that have altered effector  
CC function as a consequence of one or more amino acid modifications in the  
CC Fc region. The variant polypeptides are useful for treating cancer,  
CC allergic conditions such as asthma (with an anti-IgE antibody), and LFA-1  
CC mediated disorders. Where the polypeptide binds the HER2 receptor, the  
CC disorder preferably is HER2-expressing cancer, e.g. a benign or malignant  
CC tumour characterized by overexpression of the HER2 receptor. Such cancers  
CC include breast cancer, squamous cell cancer, small-cell lung cancer, non-  
CC small cell lung cancer, gastrointestinal cancer, pancreatic cancer,  
CC glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma,  
CC colon cancer, colorectal cancer, endometrial carcinoma, salivary gland  
CC carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer,  
CC thyroid cancer, hepatic carcinoma and various types of head and neck  
CC cancer

XX Sequence 217 AA;

Query Match 98.6%; Score 572; DB 3; Length 217;  
Best Local Similarity 98.2%; Pred. No. 3.6e-50;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60

Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 61

QY 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109

Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIKTK 110

RESULT 10

AAB76423

ID AAB76423 standard; protein; 217 AA.

XX AAB76423;

XX 10-APR-2001 (first entry)

DE Human IgG2 Fc region amino acid sequence.

XX Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia;  
KW metabolic disorder; nutritional deficiency; Alzheimer's disease;  
KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;  
KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.

OS Homo sapiens.

PN WO200101748-A2.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US019283.

XX 02-JUL-1999; 99US-0142232P.

XX (GETH ) GENENTECH INC.

XX Dennis MS;

XX WPI; 2001-123048/13.

XX Non-naturally occurring peptide ligands which compete for binding human  
PT erbB2 gene products, useful for treating e.g. Alzheimer's disease,  
PT multiple sclerosis and diabetic neuropathy.

PS Disclosure; Fig 2A; 116pp; English.

XX This invention relates to non-naturally occurring peptide ligands which  
CC bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides  
CC represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples  
CC of the ErbB2 binding ligands of the invention. Sequences AAB76421 -



```
XX SQ Sequence 217 AA;
Query Match 98.6%; Score 572; DB 5; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 109
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTSKTK 110

RESULT 13
ABR42440
ID ABR42440 standard; protein; 217 AA.
XX AC ABR42440;
XX DT 11-AUG-2003 (first entry)
XX DE Human IgG2 Fc region.
XX KW Human; antibody; IgG2; cytostatic; immunosuppressive; antiinflammatory; antimicrobial.
XX OS Homo sapiens.
XX PN W02003035835-A2.
XX PD 01-MAY-2003.
XX PF 22-OCT-2002; 2002WO-US033739.
XX PR 25-OCT-2001; 2001US-0337642P.
XX PR 09-JAN-2002; 2002US-0347694P.
XX PA (GETH ) GENENTECH INC.
XX PI Presta IG;
XX WPI; 2003-421411/39.
XX New composition comprising a glycoprotein having a Fc region useful for treating cancer, autoimmune disease, inflammatory disorder or infection in a mammal.
XX Disclosure; Fig 23; 139pp; English.
XX The present sequence is the protein sequence of the Fc region of human IgG2. A claimed composition comprises a glycoprotein having a Fc region. About 80-100% of the glycoprotein comprises a mature core carbohydrate structure which lacks fucose attached to the Fc region. The glycoprotein preferably comprises an antibody, and the Fc region is preferably a human IgG Fc region, especially a human IgG1, IgG2, IgG3 or IgG4 Fc region. The glycoprotein binds Fc gammaRIII with better affinity, or mediates antibody dependent cell-mediated cytotoxicity more effectively, than the human and binds a B-cell surface marker, an ErbB receptor, a tumour-associated antigen or an angiogenic factor, CD20, HER2, vascular endothelial growth factor, CD40 or prostate stem cell antigen. The composition is useful for treating cancer, autoimmune disease, an inflammatory disorder or infection in a mammal
XX Sequence 217 AA;

Query Match 98.6%; Score 572; DB 6; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTSKTK 110

RESULT 15
ABG31095
ID ABG31095 standard; protein; 228 AA.
XX
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Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTSKTK 110

RESULT 14
ADH75378
ID ADH75378 standard; protein; 217 AA.
XX AC ADH75378;
XX DT 22-APR-2004 (first entry)
XX DE Human IgG2.
XX KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease; human; IgG; immunoglobulin.
XX OS Homo sapiens.
XX PN US2004002587-A1.
XX PD 01-JAN-2004.
XX PF 20-FEB-2003; 2003US-00370749.
XX PR 20-FEB-2002; 2002US-0358161P.
XX PA (WATK/) WATKINS J D.
XX PA (ALLA/) ALLAN B.
XX PI Watkins JD, Allan B;
XX WPI; 2004-070755/07.
XX New composition comprising a variant of a parent polypeptide having at least a portion of a Fc region, useful in treating e.g., autoimmune diseases.
XX Disclosure; SEQ ID NO 16; 62pp; English.
XX The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the Fc region. The composition is useful in treating diseases e.g., acid autoimmune diseases. The present sequence represents the amino acid sequence of a human immunoglobulin G, IgG.
XX Sequence 217 AA;

Query Match 98.6%; Score 572; DB 8; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61

Qy 61 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
Db 62 REQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTSKTK 110

RESULT 15
ABG31095
ID ABG31095 standard; protein; 228 AA.
XX
```





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:49:37 ; Search time 17.9178 Seconds  
(without alignments)  
585.319 Million cell updates/sec

Title: US-09-674-857-2  
Perfect score: 580  
Sequence: 1 APVAGPSVFLPPPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	326	1 G2HU	Ig gamma-2 chain C
2	536	92.4	327	1 G4HU	Ig gamma-4 chain C
3	529	91.2	377	2 A23511	Ig gamma-3 chain C
4	528	91.2	377	2 A60764	Ig gamma-3 chain C
5	526	90.7	234	2 PT0207	Ig gamma chain C r
6	524	90.3	255	4 S31866	Ig gamma-1 chain C
7	524	90.3	330	1 GHU	Ig gamma-1 chain C
8	524	90.3	374	2 S69339	Ig heavy chain v r
9	516	89.0	289	1 G3HUM1	Ig gamma-3 heavy c
10	457	78.8	328	2 I47160	Ig gamma 2b chain
11	457	78.8	328	2 I47159	Ig gamma 2a chain
12	452	77.9	277	2 I47162	Ig gamma 4 chain c
13	441	76.0	328	2 I47161	Ig gamma 3 chain c
14	441	76.0	328	2 I47158	Ig gamma 1 chain c
15	429	74.0	470	2 S22080	Ig heavy chain pre
16	425	73.3	308	2 C30554	Ig heavy chain C r
17	425	73.3	329	1 G2GP	Ig gamma-2 chain C
18	425	73.3	472	2 S31459	Ig gamma-1 chain -
19	423	72.9	333	2 PS0018	Ig gamma-2b chain
20	418	72.1	323	1 GHRB	Ig gamma chain C r
21	414	71.4	327	2 S05611	Ig gamma-2 chain C
22	410.5	70.8	329	1 G3MSC	Ig gamma-3 chain C
23	410.5	70.8	398	1 G3MSM	Ig gamma-3 chain C
24	410	70.7	324	1 G1MS	Ig gamma-1 chain C
25	410	70.7	393	1 G1MSM	Ig gamma-1 chain C
26	410	70.7	444	2 PC4336	monoclonal antibody
27	400	69.0	329	2 S00847	Ig gamma-2c chain
28	384	66.2	326	2 PS0017	Ig gamma-1 chain C
29	383	66.0	335	1 G2MSAB	Ig gamma-2a chain

RESULT 1  
G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93132; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co

A:Reference number: A93906; MUID:82197621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1;

A>Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A:Reference number: A92809; MUID:81007873; PMID:6774012

A:Contents: myeloma protein Til

A:Accession: A92809

A:Molecule type: protein

A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>

A>Note: Trp-156 is at or near the complement-binding site

R:Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; MUID:80001357; PMID:113060

A:Contents: myeloma protein Zie

A:Accession: A90752

A:Molecule type: protein

A:Residues: 1-24,'E',26-57,'BV',60-85,132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198

A>Note: This sequence has since been revised

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A:Reference number: A93132; MUID:80114419; PMID:118920

A:Contents: Zie

A:Accession: A93132

A:Molecule type: protein

A:Residues: 238-275 <HOF>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidate

R:Milstien, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:127-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 98.6%; Score 572; DB 1; Length 326;  
Best Local Similarity 98.2%; Pred. No. 6.1e-50;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
Db 111 APPVAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 170

Qy 61 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIKTK 109  
Db 171 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTIKTK 219

RESULT 2  
G4HU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
C:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Cross-references: UNIPROT:P01861  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant 1  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30;81-326 <PIN>  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:127-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 92.4%; Score 536; DB 1; Length 327;  
Best Local Similarity 94.3%; Pred. No. 2.6e-46;  
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63  
Db 115 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 174

Qy 64 QFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIKTK 109  
Db 175 QFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIKTK 220

RESULT 3  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511  
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: C  
A:Reference number: A23511; MUID:86148507; PMID:3081877  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.2%; Score 529; DB 2; Length 377;  
Best Local Similarity 92.5%; Pred. No. 1.5e-45;  
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63  
Db 165 LGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 224

Qy 64 QFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTIKTK 109  
Db 225 QYNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTIKTK 270

RESULT 4  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C:Accession: A60764  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A:Reference number: A60764; MUID:90007613; PMID:2571587  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: UNIPROT:Q8N4Y9  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 91.2%; Score 529; DB 2; Length 377;  
Best Local Similarity 92.5%; Pred. No. 1.5e-45;  
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAAKTPRBE 63  
 Db 165 LGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAAKTPRBE 224  
 QY 64 QFNSTFRVSVLTVVHODWLNKGYCKVCKVSNKGLPSSIEKTIKTK 109  
 Db 225 QYNSTFRVSVLTVLHODWLNKGYCKVCKVSNKALPAPIEKTISKTK 270

RESULT 5  
 Ig gamma chain C region - chimpanzee  
 C:Species: Pan troglodytes (chimpanzee)  
 C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
 C:Accession: PT0207  
 R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
 Mol. Immunol. 28, 319-322, 1991  
 A>Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
 A:Reference number: PT0207; MUID:91287716; PMID:2062315  
 A:Accession: PT0207  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <EHR>  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 526; DB 2; Length 234;  
 Best Local Similarity 86.8%; Pred. No. 1.7e-45;  
 Matches 99; Conservative 5; Mismatches 4; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55  
 Db 21 PPCAAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 80

QY 56 AKTKPREQFNSTFRVSVLTVVHODWLNKGYCKVCKVSNKGLPSSIEKTIKTK 109  
 Db 81 AKTKPREQFNSTFRVSVLTVLHODWLNKGYCKVCKVSNKALPAPIEKTISKAK 134

RESULT 6  
 Ig gamma-1 chain C region - synthetic  
 C:Species: synthetic  
 A>Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
 C>Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
 C:Accession: S31866  
 R:Filpula, D.  
 submitted to the EMBL Data Library, February 1993  
 A:Description: Screening method for protein-protein interactions of cloned gene products.  
 A:Reference number: S31866  
 A:Accession: S31866  
 A:Molecule type: mRNA  
 A:Residues: 1-255 <FIL>  
 A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069  
 C:Keywords: immunoglobulin  
 F:1-22/Region: Escherichia coli outer membrane protein A precursor  
 F:23-255/Region: human Ig gamma-1 chain C region

Query Match 90.3%; Score 524; DB 4; Length 255;  
 Best Local Similarity 86.0%; Pred. No. 3.1e-45;  
 Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55  
 Db 35 PPCPAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 94

QY 56 AKTKPREQFNSTFRVSVLTVVHODWLNKGYCKVCKVSNKGLPSSIEKTIKTK 109  
 Db 95 AKTKPREQFNSTFRVSVLTVLHODWLNKGYCKVCKVSNKALPAPIEKTISKAK 148

RESULT 7  
 GHU

Ig gamma-1 chain C region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
 C:Accession: A93433; S36861; S36867; B90563; A90564; B91668; A91723; A02146  
 R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
 Nucleic Acids Res. 10, 4071-4079, 1982  
 A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
 A:Reference number: A93433; MUID:82274238; PMID:6287432  
 A:Accession: A93433  
 A:Molecule type: DNA  
 A:Residues: 1-330 <ELL>  
 A:Cross-references: UNIPROT:P01857; EMBL:Z17370  
 A>Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,  
 A>Note: Lys-330 is removed after translation  
 R:Harris, L.J.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S33904  
 A:Accession: S36861  
 A:Molecule type: DNA  
 A:Residues: 2-330 <HAR>  
 A:Cross-references: EMBL:Z17370  
 R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
 Cell 29, 671-679, 1982  
 A>Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
 A:Reference number: S33887; MUID:83001943; PMID:6811139  
 A:Accession: S33887  
 A:Molecule type: DNA  
 A:Residues: 88-113;235-330 <TAK>  
 A:Cross-references: EMBL:Z17370  
 R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
 Biochemistry 9, 3161-3170, 1970  
 A>Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequ  
 A:Reference number: A90563; MUID:71064024; PMID:5489771  
 A:Contents: myeloma protein Eu  
 A:Accession: B90563  
 A:Molecule type: protein  
 A:Residues: 1-96,'R',98-135 <CUN>  
 A>Note: this sequence has the G1m(3) marker, 97-Arg  
 R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
 Biochemistry 9, 3171-3181, 1970  
 A>Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ  
 A:Reference number: A90564; MUID:71064025; PMID:5530842  
 A:Contents: Eu  
 A:Accession: A90564  
 A:Molecule type: protein  
 A:Residues: 136-154,'O',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240  
 A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
 R:Ponstingl, H.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
 A>Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)  
 igen Primaerstruktur.  
 A:Reference number: A91668; MUID:77070269; PMID:826475  
 A:Contents: myeloma protein Nie  
 A:Accession: B91668  
 A:Molecule type: protein  
 A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',2,2  
 A>Note: this sequence has the G1m(17) and G1m(1) markers  
 R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
 A>Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KO  
 A:Reference number: A91723; MUID:83289131; PMID:6884994  
 A:Contents: myeloma protein KOL; disulfide bonds  
 A:Accession: A91723  
 A:Molecule type: protein  
 A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SC  
 A>Note: this sequence has the G1m(3) and G1m(non-1) markers  
 R:Gall, W.E.; Edelman, G.M.  
 Biochemistry 9, 3188-3196, 1970  
 A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
 A:Reference number: A90565; MUID:71064027; PMID:4923144  
 A:Contents: annotation; disulfide bonds  
 R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976



C.Species: Sus scrofa domestica (domestic pig)  
C.Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C.Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A.Reference number: I47158; MUID:95015845; PMID:7930579  
A.Accession: I47160  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: mRNA  
A.Residues: 1-328 <KAC>  
A.Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126  
C.Genetics:  
A.Gene: IGG2b  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:I33-202/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 457; DB 2; Length 328;  
Best Local Similarity 78.8%; Pred. No. 2.3e-38;  
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 6 GPSVFLFPKPDKDTLMISRTPEVTCTVVVDVSHEDPEVFQFNWYDGVVEHVHNAKTTPREEQF 65  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 116 GPSVFIFPPPKPDKDTLMISRTPEVTCTVVVDVSHEDPEVFQFNWYDGVVEHVHNAKTTPREEQF 175

Qy 66 NSTFRVSVLTIVHQDWLNGKEYCKVKSNKGLPSSIEKTSKTK 109  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 176 NSTYRVVSVLPIQHODWLNGKEFKCKVNKKDPAPITRIISKAK 219

RESULT 11  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C.Species: Sus scrofa domestica (domestic pig)  
C.Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C.Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A.Reference number: I47158; MUID:95015845; PMID:7930579  
A.Accession: I47159  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: mRNA  
A.Residues: 1-328 <KAC>  
A.Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
C.Genetics:  
A.Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:I33-202/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 457; DB 2; Length 328;  
Best Local Similarity 78.8%; Pred. No. 2.3e-38;  
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 6 GPSVFLFPKPDKDTLMISRTPEVTCTVVVDVSHEDPEVFQFNWYDGVVEHVHNAKTTPREEQF 65  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 116 GPSVFIFPPPKPDKDTLMISRTPEVTCTVVVDVSHEDPEVFQFNWYDGVVEHVHNAKTTPREEQF 175

Qy 66 NSTFRVSVLTIVHQDWLNGKEYCKVKSNKGLPSSIEKTSKTK 109  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 176 NSTYRVVSVLPIQHODWLNGKEFKCKVNKKDPAPITRIISKAK 219

RESULT 12  
I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C.Species: Sus scrofa domestica (domestic pig)  
C.Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C.Accession: I47162  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A.Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47162  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <KAC>  
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130  
C:Genetics:  
A:Gene: IgG4  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 452; DB 2; Length 277;  
Best Local Similarity 77.9%; Pred. No. 5.9e-38;  
Matches 81; Conservative 13; Mismatches 10; Indels 0; Gaps 0

Qy 6 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65  
Db 65 GPSAFIFPPKPKDTLMISRTPKVTCVVVDVSGENPEVQFSWYVDGVEVHNAKTRPKKEQF 124

Qy 66 NSTRRVSVLVTVVHQQDWLNGKEYCKVKSNKGLPSSIEKTIISKTK 109  
Db 125 NSTYRVSVSLPIQHQQDWLNGKEYCKVKNNKOLPAPITRIISKAK 168

RESULT 13  
I47161  
Ig gamma 3 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47161  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequence  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47161  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128  
C:Genetics:  
A:Gene: IgG3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 441; DB 2; Length 328;  
Best Local Similarity 77.9%; Pred. No. 9.2e-37;  
Matches 81; Conservative 12; Mismatches 11; Indels 0; Gaps 0

Qy 4 VAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPRE 63  
Db 114 VAGPSVIFPPKPKDITLMISQTEVTCVVVDVSKHEAEVQFSWYVDGVEVHNAETRPKEE 173

Qy 64 QFNSTFRVSVSLTVVHQQDWLNGKEYCKVKSNKGLPSSIEKTIISK 107  
Db 174 QFNSTYRVSVSLPIQHQQDWLNGKEYCKVKNNVVDLPAPITRTISK 217

RESULT 14  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequence  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47158  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122  
C:Genetics:  
A:Gene: IgG1

C.Species: Sus scrofa domestica (domestic pig)  
C.Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C.Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A.Reference number: I47158; MUID:95015845; PMID:7930579  
A.Accession: I47160  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: mRNA  
A.Residues: 1-328 <KAC>  
A.Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126  
C.Genetics:  
A.Gene: IGG2b  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:I33-202/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 457; DB 2; Length 328;  
Best Local Similarity 78.8%; Pred. No. 2.3e-38;  
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 6 GPSVFLFPKPDKDTLMISRTPEVTCTVVVDVSHEDPEVFQFNWYDGVGVHNAKTTPREEQF 65  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 116 GPSVFIFPPPKPDKDTLMISRTPTQVTCVVVDVSQENPEVQFSWYDGVGVHTAQTRPKKEQF 175

Qy 66 NSTFRVSVLTIVHQDWLNGKEYCKVKSNKGLPSSIEKTSKTK 109  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 176 NSTYRVVSVLP IQHDWLNGEKFCKVNNKDLPAPIIRIISKAK 219

RESULT 11  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C.Species: Sus scrofa domestica (domestic pig)  
C.Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C.Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A.Reference number: I47158; MUID:95015845; PMID:7930579  
A.Accession: I47159  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: mRNA  
A.Residues: 1-328 <KAC>  
A.Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
C.Genetics:  
A.Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:I33-202/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 457; DB 2; Length 328;  
Best Local Similarity 78.8%; Pred. No. 2.3e-38;  
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 6 GPSVFLFPKPDKDTLMISRTPEVTCTVVVDVSHEDPEVFQFNWYDGVGVHNAKTTPREEQF 65  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 116 GPSVFIFPPPKPDKDTLMISRTPTQVTCVVVDVSQENPEVQFSWYDGVGVHTAQTRPKKEQF 175

Qy 66 NSTFRVSVLTIVHQDWLNGKEYCKVKSNKGLPSSIEKTSKTK 109  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 176 NSTYRVVSVLP IQHDWLNGEKFCKVNNKDLPAPIIRIISKAK 219

RESULT 12  
I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C.Species: Sus scrofa domestica (domestic pig)  
C.Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C.Accession: I47162  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A.Reference number: I47158; MUID:95015845; PMID:7930579

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 79.8836 Seconds  
(without alignments)  
698.725 Million cell updates/sec

Title: US-09-674-857-2  
Perfect score: 580  
Sequence: 1 APPVAGPSVFLPPPKDPTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_prot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	326	1 GC2 HUMAN	P01859 homo sapien
2	572	98.6	417	2 Q6N093	Q6N093 homo sapien
3	572	98.6	465	2 Q6P6C4	Q6P6C4 homo sapien
4	569	98.1	464	2 Q6MZU6	Q6MZU6 homo sapien
5	563	97.1	493	2 Q68CN4	Q68CN4 homo sapien
6	539	92.9	476	2 Q6WZV7	Q6WZV7 homo sapien
7	536	92.4	327	1 GC4 HUMAN	P01861 homo sapien
8	536	92.4	473	2 Q8TC63	Q8TC63 homo sapien
9	532	91.7	509	2 Q8NF17	Q8NF17 homo sapien
10	532	91.7	521	2 Q8N4Y9	Q8N4Y9 homo sapien
11	529	91.2	354	2 Q86TT2	Q86TT2 homo sapien
12	529	91.2	518	2 Q6N030	Q6N030 homo sapien
13	524	90.3	330	1 GC1 HUMAN	P01857 homo sapien
14	524	90.3	348	2 Q6PFX1	Q6PFX1 homo sapien
15	524	90.3	465	2 Q6GKX6	Q6GKX6 homo sapien
16	524	90.3	466	2 Q6IN78	Q6IN78 homo sapien
17	524	90.3	469	2 Q727P5	Q727P5 homo sapien
18	524	90.3	470	2 Q6PJA4	Q6PJA4 homo sapien
19	524	90.3	470	2 Q725W1	Q725W1 homo sapien
20	524	90.3	472	2 Q6N089	Q6N089 homo sapien
21	524	90.3	473	2 Q6MZV7	Q6MZV7 homo sapien
22	524	90.3	473	2 Q6P055	Q6P055 homo sapien
23	524	90.3	475	2 Q6GMW7	Q6GMW7 homo sapien
24	524	90.3	475	2 Q6MZQ6	Q6MZQ6 homo sapien
25	524	90.3	475	2 Q6N095	Q6N095 homo sapien
26	524	90.3	476	2 Q6GKX1	Q6GKX1 homo sapien
27	524	90.3	478	2 Q6P181	Q6P181 homo sapien
28	524	90.3	480	2 Q6N094	Q6N094 homo sapien
29	524	90.3	480	2 Q6P1F1	Q6P1F1 homo sapien
30	524	90.3	481	2 Q6N097	Q6N097 homo sapien
31	524	90.3	482	2 Q72351	Q72351 homo sapien

32	524	90.3	544	2	Q6PJ95	Q6PJ95 homo sapien
33	524	90.3	679	2	Q96PQ8	Q96PQ8 homo sapien
34	521	89.8	466	2	Q6N096	Q6N096 homo sapien
35	519	89.5	487	2	Q65ZL2	Q65ZL2 mus sp. fv/
36	516	89.0	290	1	GC3 HUMAN	P01860 homo sapien
37	443	76.4	337	2	Q95M34	Q95M34 equus cabal
38	435	73.3	329	1	GC2 CAVPO	P01862 cavia porce
39	423	72.9	333	1	GC5 RAT	P20761 rattus norv
40	418	72.1	323	1	GC_RABIT	P01870 oryctolagus
41	410.5	70.8	303	2	Q6KAM2	Q6KAM2 mus musculu
42	410.5	70.8	329	1	GC3 MOUSE	P22436 mus musculu
43	410.5	70.8	398	1	GC3M MOUSE	P03987 mus musculu
44	410.5	70.8	470	2	Q7TMK1	Q7TMK1 mus musculu
45	410	70.7	324	1	GC1_MOUSE	P01868 mus musculu

## ALIGNMENTS

RESULT 1  
GC2\_HUMAN STANDARD; PRT; 326 AA.  
ID GC2\_HUMAN  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig gamma-2 chain C region.  
GN Name=IGHG2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellison J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy  
chain constant region genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;  
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for  
evolution of a gene family.";  
RN [3]  
RL Cell 29:671-679(1982).  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
genes.";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
evolutionary, and functional implications.";  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=80001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
domains of a human IgG2 myeloma protein.";  
RN [6]  
RL Can. J. Biochem. 57:758-767(1979).  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;

RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
RL immunoglobulins gamma chains.";  
RM Mol. Immunol. 16:923-925 (1979).  
[7]  
RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
RA Hofmann T., Parr D.M.;  
RL Submitted (MAR-1980) to the PIR data bank.  
[8]  
RN SEQUENCE OF 1-121 (DOT).  
RX MEDLINE=9525298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
RL immunoglobulins.";  
RM Eur. J. Biochem. 228:886-893 (1995).  
[9]  
RN DISULFIDE BONDS.  
RX MEDLINE=72033500; PubMed=4940472;  
RA Milestein C., Frangione B.;  
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
RM Biochem. J. 121:217-225 (1971).  
[10]  
RN DISULFIDE BONDS.  
RX MEDLINE=69064124; PubMed=5782707;  
RA Frangione B., Milestein C., Pink J.R.L.;  
RT "Structural studies of immunoglobulin G.";  
RM Nature 221:145-148 (1969).  
CC -----  
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CC -----  
DR EMBL; J00230; AAB59393.1; -.  
DR PIR; A3906; G2HU.  
DR HSP; P01857; 100K.  
DR Genew; HGNC:5526; IHG2.  
DR MIM; 147110; -.  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; P:antigen binding; TAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-Like.  
DR InterPro; IPR003597; IG-cl.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS50835; IG-LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
DR Direct protein sequencing; Immunoglobulin C region;  
KW Immunoglobulin domain.  
FT NON\_TER 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 Hinge.  
FT DOMAIN 111 219 CH2.  
FT DOMAIN 220 326 CH3.  
FT DISULFID 14 14 Interchain (with a light chain).  
FT DISULFID 27 83 Interchain (with a heavy chain).  
FT DISULFID 102 102 Interchain (with a heavy chain).  
FT DISULFID 103 103 Interchain (with a heavy chain).  
FT DISULFID 106 106 Interchain (with a heavy chain).  
FT DISULFID 109 109 Interchain (with a heavy chain).  
FT DISULFID 140 200  
FT DISULFID 246 304  
FT SITE 156 156  
FT VARIANT 60 60  
FT CONFLICT 109 109 At or near the complement-binding site.  
FT CONFLICT 326 AA; 35884 MW; 8310878C6878CF9C CRC64; S -> A (in myeloma proteins TIL and ZIE).  
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64; FTIG=VAR\_003889.  
C -> S (in Ref. 3).  
SQ  
Query Match 98.6%; Score 572; DB 1; Length 326;

Best Local Similarity 98.2%; Pred. No. 5.5e-49;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
DB 111 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 170  
QY 61 REEFNSTFRVSVLTVVHQDLNGKEYCKVKSNKGLPSSIEKTIKTK 109  
DB 171 REEFNSTFRVSVLTVVHQDLNGKEYCKVKSNKGLPAPIEKTIKTK 219  
RESULT 2  
QGN093 PRELIMINARY; PRT; 417 AA.  
AC Q6N093;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686I04196 (Fragment).  
GN Name=DKFZp686I04196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiegmann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640623; CAE45777.1; -.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
FT NON\_TER 1  
FT SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;  
Query Match 98.6%; Score 572; DB 2; Length 417;  
Best Local Similarity 98.2%; Pred. No. 7.3e-49;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
DB 202 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 261  
QY 61 REEFNSTFRVSVLTVVHQDLNGKEYCKVKSNKGLPSSIEKTIKTK 109  
DB 262 REEFNSTFRVSVLTVVHQDLNGKEYCKVKSNKGLPAPIEKTIKTK 310  
RESULT 3  
Q6P6C4 PRELIMINARY; PRT; 465 AA.  
AC Q6P6C4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
RA Altschul S.F., Zebberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnorch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC062335; AAH62335.1; -;  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51325 MW; FDB9348ADC37B6D CRC64;  
  
Query Match 98.6%; Score 572; DB 2; Length 465;  
Best Local Similarity 98.2%; Pred. No. 8.2e-49;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKP 60  
Db 250 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKP 309  
  
QY 61 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109  
Db 310 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPAPIKTIKTK 358  
  
RESULT 4  
Q6MZU6 PRELIMINARY; PRT; 464 AA.  
ID Q6MZU6  
AC Q6MZU6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686C15213.  
GN Name=DKFZp686C15213;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640874; CAE45931.1; -;  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C6688A0ABC CRC64;  
  
Query Match 98.1%; Score 569; DB 2; Length 464;  
Best Local Similarity 97.2%; Pred. No. 1.6e-48;  
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKP 60  
Db 249 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKP 308  
  
QY 61 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109  
Db 309 REEQFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPAPIKTIKTK 357  
  
RESULT 5  
Q68CN4 PRELIMINARY; PRT; 493 AA.  
ID Q68CN4  
AC Q68CN4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein DKFZp686E23209 (Fragment).  
GN Name=DKFZp686E23209;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Rectum tumor;  
RG The German cDNA Consortium;  
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,  
RA Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR749861; CAH18705.1; -;  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 493 AA; 54117 MW; A1B4F5ED3FABAB40 CRC64;  
  
Query Match 97.1%; Score 563; DB 2; Length 493;

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Best Local Similarity 96.3%; Pred. No. 7e-48;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 60
Db 278 APPVAGPSAFLPPPKPNDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 337

QY 61 REEQFNSTFRVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109
Db 338 REEQFNSTFRVSVLTVVHODWLNGKEYKCKVSNKGLPAPIEKTISKTK 386

RESULT 6
Q6MZX7
ID Q6MZX7 PRELIMINARY; PRT; 476 AA.
AC Q6MZX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686M24218.
GN Name=DKFZp686M24218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640824; CAE45900.1; -.
DR HSP; F01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FFE5853958F CRC64;

Query Match 92.9%; Score 539; DB 2; Length 476;
Best Local Similarity 95.3%; Pred. No. 1.7e-45;
Matches 101; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTPREE 63
Db 264 LGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTPREE 323

QY 64 QFNSTFRVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109
Db 324 QFNSTFRVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTIISKTK 369

RESULT 7
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-4 chain C region.
GN Name=IGHG4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
CC -----
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; IADO; X-ray; A=118-323.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
DR 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 1 98
FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 220
FT DOMAIN 221 327
FT DISULFID 14 14
FT DISULFID 27 83 Interchain (with a light chain).
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 92.4%; Score 536; DB 1; Length 327;
Best Local Similarity 94.3%; Pred. No. 2.2e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTPREE 63
Db 115 LGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTPREE 174

QY 64 QFNSTFRVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109
Db 175 QFNSTFRVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTIISKTK 220

RESULT 8
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003196; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 92.4%; Score 536; DB 2; Length 473;
Best Local Similarity 94.3%; Pred. NO. 3.4e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
Db 261 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 320

QY 64 QFNSTFRVSVLTIVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 321 QFNSTFRVSVLTIVHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAK 366

RESULT 9
Q8NF17 PRELIMINARY; PRT; 509 AA.
AC Q8NF17
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLJ00385 protein (Fragment).
GN Name=FLJ00385;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090464; BAC03445.1; -.
DR PIR; A45874; A45874.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 509 AA; 56110 MW; 089498D8076E863C CRC64;

Query Match 91.7%; Score 532; DB 2; Length 509;
Best Local Similarity 93.4%; Pred. NO. 9.2e-45;
Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
Db 228 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 287

QY 64 QFNSTFRVSVLTIVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 288 QFNSTFRVSVLTIVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 333

RESULT 10
Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC033178; AAH33178.1; -.
DR PIR; A60764; A60764.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match          91.7%; Score 532; DB 2; Length 521;
Best Local Similarity 93.4%; Pred. No. 9.5e-45;
Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DQ 309 LGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 368
QY 64 QFNSTFRVSVLTIVHQLWLNKGYCKVSNKGLPSSIEKTIKTK 109
DQ 369 QFNSTFRVSVLTIVHQLWLNKGYCKVSNKGLPSSIEKTIKTK 414

RESULT 11
ID Q86TT2 PRELIMINARY; PRT; 354 AA.
AC Q86TT2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0D1019F20 of Placenta of Homo sapiens
DE (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Placenta;
RC Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE=Placenta;
RC Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248278; CAD62606.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 354 AA; 39125 MW; 23B80BF4D2B87A92 CRC64;

Query Match          91.2%; Score 529; DB 2; Length 354;
Best Local Similarity 92.5%; Pred. No. 1.2e-44;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DQ 142 LGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 201
QY 64 QFNSTFRVSVLTIVHQLWLNKGYCKVSNKGLPSSIEKTIKTK 109
DQ 202 QYNSTFRVSVLTIVHQLWLNKGYCKVSNKGLPSSIEKTIKTK 247

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RESULT 12
Q6N030 PRELIMINARY; PRT; 518 AA.
ID Q6N030;
AC Q6N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFP686115212.
GN Name=DKFP686115212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Meves H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match          91.2%; Score 529; DB 2; Length 518;
Best Local Similarity 92.5%; Pred. No. 1.9e-44;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DQ 306 LGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 365
QY 64 QFNSTFRVSVLTIVHQLWLNKGYCKVSNKGLPSSIEKTIKTK 109
DQ 366 QYNSTFRVSVLTIVHQLWLNKGYCKVSNKGLPSSIEKTIKTK 411

RESULT 13
GCI_HUMAN STANDARD; PRT; 330 AA.
ID GCI_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IG gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human;
RC Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE=Human;
RC Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

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RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";   
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino  
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";   
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic  
RT peptides of the H-chain, alignment of the tryptic peptides and  
RT discussion of the complete structure.";   
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary  
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";   
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RT Intrachain disulfide bonds.";   
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges.";   
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";   
RL Biochemistry 20:2361-2370(1981).  
CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the  
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
CC G1M(3) marker and the G1M (non-1) markers.  
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A93433; GHU.  
DR PDB; 1AJ7; X-ray; H=1-103.  
DR PDB; 1D5B; X-ray; B/H=1-101.  
DR PDB; 1D5I; X-ray; H=1-101.  
DR PDB; 1D6V; X-ray; H=1-101.  
DR PDB; 1DN2; X-ray; A/B=120-326.  
DR PDB; 1E4K; X-ray; A/B=106-329.  
DR PDB; 1FC1; X-ray; A/B=106-329.  
DR PDB; 1FC2; X-ray; D=106-329.  
DR PDB; 1FCC; X-ray; A=121-326.  
DR PDB; 1H2H; X-ray; H/K=1-330.  
DR PDB; 1I7Z; X-ray; B/D=1-103.  
DR PDB; 1IIS; X-ray; A/B=107-330.  
DR PDB; 1IIX; X-ray; A/B=107-330.  
DR PDB; 1L6X; X-ray; A=120-326.  
DR PDB; 1LOX; X-ray; A/B=119-330.  
DR PDB; 2RCS; X-ray; H=1-103.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM; 147100; -.  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; F:antigen binding; TAS.  
DR GO; GO:0008955; P:immune response; NAS.  
DR InterPro; IPR007110; I9-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; I9; 3.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW 3D-structure; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 Hinge.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83 Interchain (with light chain).  
FT DISULFID 103 103 Interchain (with heavy chain).  
FT DISULFID 109 109 Interchain (with heavy chain).  
FT DISULFID 112 112 Interchain (with heavy chain).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180 N-linked (GlcNAc...).  
FT VARIANT 239 239 K -> R (in G1M(3) marker).  
FT VARIANT 241 241 /FTIG=VAR\_003886.  
FT STRAND 23 24 D -> E (in G1M(non-1) marker).  
FT STRAND 26 33 /FTIG=VAR\_003887.  
FT STRAND 38 38 L > M (in G1M(non-1) marker).  
FT STRAND 41 41 /FTIG=VAR\_003888.  
FT TURN 42 45  
FT TURN 48 49  
FT STRAND 50 52  
FT STRAND 57 58  
FT TURN 59 61  
FT STRAND 62 71  
FT HELIX 73 75  
FT TURN 76 78  
FT TURN 82 87  
FT TURN 88 91  
FT STRAND 92 97  
FT TURN 102 103  
FT STRAND 122 126  
FT HELIX 130 134  
FT TURN 136 137  
FT STRAND 141 149  
FT STRAND 157 162  
FT TURN 163 164  
FT STRAND 165 167  
FT STRAND 171 171

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FT STRAND 176 177
FT TURN 179 180
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 245 256
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FT TURN 267 268
FT STRAND 270 270
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FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 311
FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 90.3%; Score 524; DB 1; Length 330;
Best Local Similarity 86.0%; Pred. No. 3.6e-44;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVVHN 55
DB 110 PCPAPELGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVVHN 169

QY 56 AKTPREEQFNSTRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIISKTK 109
DB 170 AKTPREEQYNSTRVSVLTVLHQDNLGKEYCKVSNKALPAPIEKTISKAK 223

RESULT 14
O6PYX1
ID Q6PYX1 PRELIMINARY; PRT; 348 AA.
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu N.S., Chen Y.Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570731; AAS88328.1; -.
DR HSP; P01857; IAJ7.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Receptor.
FT NON_TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0B5E845 CRC64;

Query Match 90.3%; Score 524; DB 2; Length 348;
Best Local Similarity 86.0%; Pred. No. 3.8e-44;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVVHN 55
DB 110 PCPAPELGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVVHN 169

QY 56 AKTPREEQFNSTRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIISKTK 109
DB 170 AKTPREEQYNSTRVSVLTVLHQDNLGKEYCKVSNKALPAPIEKTISKAK 223

RESULT 15
Q6GMX6
ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 90.3%; Score 524; DB 2; Length 465;
Best Local Similarity 86.0%; Pred. No. 5.3e-44;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVVHN 55
DB 110 PCPAPELGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDDEVQFNWYVDGVVHN 187

QY 56 AKTPREEQFNSTRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIISKTK 109
DB 188 AKTPREEQYNSTRVSVLTVLHQDNLGKEYCKVSNKALPAPIEKTISKAK 241
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Db 245 PPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 304

Qy 56 AKTKPREQFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPSSIEKTIKTK 109

Db 305 AKTKPREQVNSTYRVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTIKRAK 358

Search completed: November 17, 2005, 07:10:19  
Job time : 79.8836 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:51:22 ; Search time 24.3881 Seconds  
(without alignments)  
333.636 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGPSVFLFPPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	99.5	448	4	US-09-968-362A-18
2	572	98.6	109	3	US-08-444-644-30
3	572	98.6	109	3	US-08-232-246A-30
4	572	98.6	217	4	US-09-483-588-5
5	572	98.6	228	4	US-09-968-362A-27
6	572	98.6	432	3	US-08-477-460B-2
7	572	98.6	432	3	US-08-379-516-2
8	572	98.6	432	3	US-09-329-916-2
9	572	98.6	432	3	US-08-485-372A-2
10	572	98.6	432	3	US-09-409-006A-2
11	572	98.6	432	4	US-08-484-681-2
12	572	98.6	432	4	US-09-766-995-2
13	572	98.6	432	5	PCT-US93-07422-2
14	572	98.6	451	4	US-09-472-087-70
15	572	98.6	463	4	US-09-472-087-1
16	572	98.6	463	4	US-09-472-087-4
17	572	98.6	463	4	US-09-472-087-63
18	572	98.6	463	4	US-09-472-087-68
19	572	98.6	464	4	US-09-472-087-2
20	572	98.6	464	4	US-09-472-087-66
21	572	98.6	470	4	US-09-859-053-28
22	572	98.6	470	4	US-09-859-053-32
23	572	98.6	470	4	US-09-859-053-36
24	572	98.6	530	3	US-08-477-460B-4
25	572	98.6	530	3	US-08-379-516-4
26	572	98.6	530	3	US-08-329-916-4
27	572	98.6	530	3	US-08-485-372A-4

28	572	98.6	530	3	US-09-409-006A-4	Sequence 4, Appli
29	572	98.6	530	4	US-08-484-681-4	Sequence 4, Appli
30	572	98.6	530	4	US-09-766-995-4	Sequence 4, Appli
31	572	98.6	530	5	PCT-US93-07422-4	Sequence 4, Appli
32	569	98.1	450	2	US-08-788-800-12	Sequence 12, Appl
33	569	98.1	469	2	US-07-934-373C-23	Sequence 23, Appl
34	569	98.1	469	3	US-08-437-642B-23	Sequence 23, Appl
35	569	98.1	469	4	US-08-146-206C-23	Sequence 23, Appl
36	569	98.1	469	4	US-09-705-686-23	Sequence 23, Appl
37	569	98.1	469	4	US-09-705-392A-23	Sequence 23, Appl
38	569	98.1	469	4	US-09-705-398-23	Sequence 23, Appl
39	569	98.1	552	5	PCT-US93-07832-23	Sequence 23, Appl
40	566	97.6	463	4	US-09-472-087-64	Sequence 64, Appl
41	562	96.9	326	2	US-08-656-886-9	Sequence 9, Appli
42	562	96.9	462	4	US-09-627-896B-24	Sequence 24, Appl
43	537.5	92.7	449	4	US-09-968-362A-20	Sequence 20, Appli
44	536	92.4	109	2	US-08-070-116A-4	Sequence 4, Appli
45	536	92.4	109	4	US-08-557-050-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-968-362A-18

; Sequence 18, Application US/09968362A

; Patent No. 6797493

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor

; TITLE OF INVENTION: increased biological activities

; FILE REFERENCE: 03SUN2001

; CURRENT APPLICATION NUMBER: US/09/968.362A

; CURRENT FILING DATE: 2001-10-01

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 18

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: hG-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure

; OTHER INFORMATION: 2A)

US-09-968-362A-18

Query Match 99.5%; Score 577; DB 4; Length 448;

Best Local Similarity 99.1%; Pred. No. 2.7e-59;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

Db 233 APPVAGPSVFLFPPKPKDTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 292

Qy 61 REQFNSTFRVSVLTIVVHQDLNGKEYCKVSNKGLPSSIEKTIKTK 109

Db 293 REQFNSTFRVSVLTIVVHQDLNGKEYCKVSNKGLPSSIEKTIKTK 341

RESULT 2

US-08-444-644-30

; Sequence 30, Application US/08444644

; Patent No. 6015555

; GENERAL INFORMATION:

; APPLICANT: Friden, Phillip M.

; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

; TITLE OF INVENTION: CONJUGATES

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

```
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/444,644
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1989
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match          98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPAPIEKTIKTK 109

RESULT 3
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/232,246A
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-30

Query Match          98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPAPIEKTIKTK 109

RESULT 4
US-09-483-588-5
; Sequence 5, Application US/09483588
; Patent No. 6737056
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; FILE REFERENCE: P1726R1
; CURRENT APPLICATION NUMBER: US/09/483,588
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: US 60/116,023
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-483-588-5

Query Match          98.6%; Score 572; DB 4; Length 217;
Best Local Similarity 98.2%; Pred. No. 4.1e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61
QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
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Db 62 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 110
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RESULT 5
US-09-968-362A-27
; Sequence 27, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUM2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Human IgG2 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-27

Query Match 98.6%; Score 572; DB 4; Length 228;
Best Local Similarity 98.2%; Pred. No. 4.4e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 60
Db 13 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 72
Qy 61 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTISKTK 109
Db 73 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 121

RESULT 6
US-09-477-460B-2
; Sequence 2, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
```

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; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-477-460B-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 60
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 276
Qy 61 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTISKTK 109
Db 277 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 325

RESULT 7
US-08-379-516-2
; Sequence 2, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
; TITLE OF INVENTION: Immunoconjugates and Uses Thereof
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; CURRENT FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; EARLIER FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-2

Query Match 98.6%; Score 572; DB 3; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 276
Qy 61 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPSSIEKTISKTK 109
Db 277 REEQNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIEKTISKTK 325

RESULT 8
US-09-329-916-2
; Sequence 2, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/329,916  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,460  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-09-329-916-2

Query Match 98.6%; Score 572; DB 3; Length 432;  
Best Local Similarity 98.2%; Pred. No. 1e-58;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDMLISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
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Db 217 APPVAGSVLFPKPKDMLISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 276  
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QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTSKTK 109  
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RESULT 9  
US-08-485-372A-2  
Sequence 2, Application US/08485372A  
Patent No. 6187748  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,372A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,227  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-II-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-485-372A-2

Query Match 98.6%; Score 572; DB 3; Length 432;  
Best Local Similarity 98.2%; Pred. No. 1e-58;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFPKPKDMLISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
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Db 217 APPVAGSVLFPKPKDMLISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 276  
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QY 61 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTSKTK 109  
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Db 277 REEQFNSTFRVSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTK 325  
|||||

RESULT 10  
US-09-409-006A-2  
Sequence 2, Application US/09409006A  
Patent No. 6342586  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/409,006A  
FILING DATE: 29-SEP-1999  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-09-409-006A-2

Query Match 98.6%; Score 572; DB 3; Length 432;  
Best Local Similarity 98.2%; Pred. No. 1e-58;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60  
Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276  
Qy 61 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPSSIEKTIKTK 109  
Db 277 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPAPIEKTIKTK 325

RESULT 11

US-08-484-681-2  
Sequence 2, Application US/08484681  
Patent No. 6451313  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,681  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-11-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-484-681-2

Query Match 98.6%; Score 572; DB 4; Length 432;  
Best Local Similarity 98.2%; Pred. No. 1e-58;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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Db 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276  
Qy 61 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPSSIEKTIKTK 109  
Db 277 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPAPIEKTIKTK 325

RESULT 12

US-09-766-995-2  
Sequence 2, Application US/09766995  
Patent No. 6737267  
GENERAL INFORMATION:  
APPLICANT: Graham P. Allaway et al.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF  
FILE REFERENCE: 2048/41315-CB/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/766,995  
CURRENT FILING DATE: 2001-01-22  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 432  
TYPE: PRT  
ORGANISM: homo sapians  
US-09-766-995-2

Query Match 98.6%; Score 572; DB 4; Length 432;  
Best Local Similarity 98.2%; Pred. No. 1e-58;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60  
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Qy 61 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPSSIEKTIKTK 109  
Db 277 REEQFNSTFRVSVLTVVHODWLNKKEYCKVSNKGLPAPIEKTIKTK 325

RESULT 13

PCT-US93-07422-2  
Sequence 2, Application PC/TUS9307422  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07422  
FILING DATE: 19930806  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 07/927,931  
APPLICATION NUMBER: 07-AUG-1992

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; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; PCT-US93-07422-2

Query Match      98.6%; Score 572; DB 5; Length 432;
Best Local Similarity 98.2%; Pred. No. 1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
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Qy 61 REEQFNSTFRVSVSLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
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RESULT 14
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-70

Query Match      98.6%; Score 572; DB 4; Length 451;
Best Local Similarity 98.2%; Pred. No. 1.1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
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Qy 61 REEQFNSTFRVSVSLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
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RESULT 15

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US-09-472-087-1
; Sequence 1, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-1

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Best Local Similarity 98.2%; Pred. No. 1.1e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 61 REEQFNSTFRVSVSLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

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Title: US-09-674-857-2

Perfect score: 580

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Searched: 1867879 seqs, 418409474 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	577	99.5	436	10 US-09-932-812-18	Sequence 18, Appl
3	577	99.5	436	16 US-10-761-593A-18	Sequence 18, Appl
4	577	99.5	436	20 US-11-016-518A-18	Sequence 18, Appl
5	577	99.5	436	20 US-11-017-185-18	Sequence 18, Appl
6	577	99.5	448	10 US-09-968-362-18	Sequence 18, Appl
7	577	99.5	448	16 US-10-800-497-18	Sequence 18, Appl
8	577	99.5	448	16 US-10-800-449-18	Sequence 18, Appl
9	572	98.6	109	18 US-10-959-318-2	Sequence 2, Appl
10	572	98.6	217	9 US-09-813-341-3	Sequence 3, Appl
11	572	98.6	217	14 US-10-277-370-3	Sequence 3, Appl

12	572	98.6	217	14	US-10-196-394-74	Sequence 74, Appl
13	572	98.6	217	15	US-10-370-749-16	Sequence 16, Appl
14	572	98.6	217	16	US-10-835-642-5	Sequence 5, Appl
15	572	98.6	217	16	US-10-757-863-5	Sequence 5, Appl
16	572	98.6	217	17	US-10-982-470-5	Sequence 5, Appl
17	572	98.6	217	20	US-11-158-839-5	Sequence 5, Appl
18	572	98.6	228	15	US-10-466-593-3	Sequence 3, Appl
19	572	98.6	228	16	US-10-761-593A-27	Sequence 27, Appl
20	572	98.6	228	16	US-10-800-449-27	Sequence 27, Appl
21	572	98.6	228	16	US-10-800-449-27	Sequence 27, Appl
22	572	98.6	228	20	US-11-016-518A-27	Sequence 27, Appl
23	572	98.6	228	20	US-11-017-185-27	Sequence 27, Appl
24	572	98.6	310	16	US-10-684-109-75	Sequence 75, Appl
25	572	98.6	326	13	US-10-047-542-22	Sequence 22, Appl
26	572	98.6	326	14	US-10-310-719-9	Sequence 9, Appl
27	572	98.6	326	15	US-10-112-582-2	Sequence 28, Appl
28	572	98.6	326	15	US-10-038-591-28	Sequence 28, Appl
29	572	98.6	326	15	US-10-656-769-6	Sequence 6, Appl
30	572	98.6	326	16	US-10-775-444A-28	Sequence 28, Appl
31	572	98.6	326	16	US-10-756-153-32	Sequence 32, Appl
32	572	98.6	326	17	US-10-872-932A-37	Sequence 37, Appl
33	572	98.6	326	17	US-10-928-305-8	Sequence 8, Appl
34	572	98.6	326	17	US-10-891-658-4	Sequence 4, Appl
35	572	98.6	326	17	US-10-893-576-46	Sequence 46, Appl
36	572	98.6	326	18	US-10-810-881A-36	Sequence 36, Appl
37	572	98.6	326	18	US-10-981-936-36	Sequence 36, Appl
38	572	98.6	326	20	US-11-001-980-6	Sequence 2, Appl
39	572	98.6	326	20	US-11-001-980-6	Sequence 6, Appl
40	572	98.6	326	20	US-11-004-054-4	Sequence 4, Appl
41	572	98.6	326	20	US-11-026-998-23	Sequence 23, Appl
42	572	98.6	326	20	US-11-027-309A-23	Sequence 23, Appl
43	572	98.6	432	8	US-08-485-163-3	Sequence 3, Appl
44	572	98.6	432	9	US-09-766-995-2	Sequence 2, Appl
45	572	98.6	442	20	US-11-034-655-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-10-745-775-16  
; Sequence 16, Application US/10745775  
; Publication No. US20040237124A1  
; GENERAL INFORMATION:  
; APPLICANT: Pons, Jaume  
; TITLE OF INVENTION: ANTI-NGF ANTIBODIES AND METHODS USING  
; TITLE OF INVENTION: SAME  
; FILE REFERENCE: 514712001400  
; CURRENT APPLICATION NUMBER: US/10745,775  
; CURRENT FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: US 60/436,905  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: US 60/443,522  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 60/510,006  
; PRIOR FILING DATE: 2003-10-08  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16,  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-745-775-16

Query Match 100.0%; Score 580; DB 16; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.3e-48;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPPKPKDTLMIKRTPEVTCTVVDVSHEDPEVQFNWYVDGVENAKTKP 60  
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Db 232 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVGVHNAKTKP 291  
Qy 61 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109  
Db 292 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 340  
RESULT 2  
US-09-932-812-18  
; Sequence 18, Application US/09932812  
; Publication No. US20030082749A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity  
; FILE REFERENCE: 02SUN2001  
; CURRENT APPLICATION NUMBER: US/09/932,812  
; CURRENT FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: A)  
US-09-932-812-18  
Query Match 99.5%; Score 577; DB 10; Length 436;  
Best Local Similarity 99.1%; Pred. No. 2.4e-48;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVGVHNAKTKP 60  
Db 221 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVGVHNAKTKP 280  
Qy 61 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109  
Db 281 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 329  
RESULT 3  
US-10-761-593A-18  
; Sequence 18, Application US/10761593A  
; Publication No. US20040175824A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological activity  
; FILE REFERENCE: 02SUN2001-A  
; CURRENT APPLICATION NUMBER: US/10/761,593A  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: 09/932812  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: 2A)  
US-10-761-593A-18  
Query Match 99.5%; Score 577; DB 16; Length 436;  
Best Local Similarity 99.1%; Pred. No. 2.4e-48;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVGVHNAKTKP 60  
Db 221 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVGVHNAKTKP 280  
Qy 61 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109  
Db 281 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 329  
RESULT 4  
US-11-016-518A-18  
; Sequence 18, Application US/11016518A  
; Publication No. US20050124045A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity  
; FILE REFERENCE: 02SUN2004D1  
; CURRENT APPLICATION NUMBER: US/11/016,518A  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US 09/932,812  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: 2A)  
US-11-016-518A-18  
Query Match 99.5%; Score 577; DB 20; Length 436;  
Best Local Similarity 99.1%; Pred. No. 2.4e-48;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVGVHNAKTKP 60  
Db 221 APPVAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVGVHNAKTKP 280  
Qy 61 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109  
Db 281 REEQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 329  
RESULT 5  
US-11-017-185-18  
; Sequence 18, Application US/11017185  
; Publication No. US20050142642A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity  
; FILE REFERENCE: 02SUN2001D2  
; CURRENT APPLICATION NUMBER: US/11/017,185  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US 09/932,812  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: A)  
US-11-017-185-18

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Query Match          99.5%; Score 577; DB 20; Length 436;
Best Local Similarity 99.1%; Pred. No. 2.4e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
    |||||
Db 221 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 280

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 281 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 329

RESULT 6
US-09-968-362-18
; Sequence 18, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-09-968-362-18

Query Match          99.5%; Score 577; DB 10; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
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Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 7
US-10-800-497-18
; Sequence 18, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; TITLE OF INVENTION: stimulating factor with
; FILE REFERENCE: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-800-497-18

Query Match          99.5%; Score 577; DB 10; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
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Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 8
US-10-800-449-18
; Sequence 18, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-800-449-18

Query Match          99.5%; Score 577; DB 16; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
    |||||
Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 9
US-10-959-318-2
; Sequence 2, Application US/10959318
; Publication No. US20050215769A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-959-318-2
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; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader
; OTHER INFORMATION: peptide (Figure
; OTHER INFORMATION: 2A)
US-10-800-497-18

Query Match          99.5%; Score 577; DB 16; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
    |||||
Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 8
US-10-800-449-18
; Sequence 18, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-800-449-18

Query Match          99.5%; Score 577; DB 16; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
    |||||
Db 233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 292

Qy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
    |||||
Db 293 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPASIETISKTK 341

RESULT 9
US-10-959-318-2
; Sequence 2, Application US/10959318
; Publication No. US20050215769A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure
US-10-959-318-2
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[illegible]

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Oy 1 APPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61
Oy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIISKTK 110
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## RESULT 14

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US-10-835-642-5
; Sequence 5, Application US/10835642
; Publication No. US20040191244A1
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; FILE REFERENCE: P1726R1
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; CURRENT APPLICATION NUMBER: US/10/835,642
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/483,588
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/116,023
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-835-642-5
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Query Match 98.6%; Score 572; DB 16; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Oy 1 APPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61
Oy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIISKTK 110
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## RESULT 15

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US-10-757-863-5
; Sequence 5, Application US/10757863
; Publication No. US20040228856A1
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; FILE REFERENCE: P1726R1
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; CURRENT APPLICATION NUMBER: US/10/757,863
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/483,588
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/116,023
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-757-863-5
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Query Match 98.6%; Score 572; DB 16; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Oy 1 APPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 2 APPVAGPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 61
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Oy 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
Db 62 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIISKTK 110
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Search completed: November 17, 2005, 07:37:35  
Job time : 84.6164 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.0913 Seconds  
(without alignments)  
473.187 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGSVFLPPPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	98.6	109	2	AAR41709
2	572	98.6	109	3	AAY54997
3	562	96.9	109	3	AAY54996
4	540.5	93.2	110	3	AAY54998
5	536	92.4	109	2	AAR67438
6	536	92.4	110	2	AAR41717
7	523	90.2	109	7	ADD25659
8	523	90.2	110	2	AAR27680
9	523	90.2	110	2	AAR41684
10	523	90.2	110	8	ADH75385
11	522	90.0	102	8	ADJ52132
12	522	90.0	105	2	ADY42626
13	518	89.3	109	5	AAE28089
14	518	89.3	110	8	ADH75415
15	517	89.1	110	8	ADL90103
16	516	89.0	110	8	ADH75413
17	515	88.8	109	7	ADD25761
18	514	88.6	110	2	AAR41713
19	509	87.8	102	8	ADJ52129
20	408	70.3	110	2	AAW71023
21	383	66.0	110	1	AAP83207
22	347	59.8	72	8	ADL15711
23	321	55.3	66	2	AAR75349
24	321	55.3	66	2	AAR75351
25	309	53.3	76	8	ADL15713

ALIGNMENTS									
RESULT 1									
AAR41709									
ID	AAR41709	standard; protein; 109 AA.							
XX	AC	AAR41709;							
XX	DT	25-MAR-2003 (revised)							
DT	20-OCT-1993	(first entry)							
XX	DE	Undefined ORF2 encoded by plasmid pAH4625.							
XX	KW	Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807;							
KW	KW	transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;							
KW	KW	endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;							
KW	KW	diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;							
KW	KW	Parkinsons disease; Alzheimers disease; SP2/0 cell.							
OS	OS	Synthetic.							
XX	XX	WO9310819-A1.							
PN	PN	10-JUN-1993.							
PD	PD	24-NOV-1992; 92WO-US010206.							
XX	XX	26-NOV-1991; 91US-00800458.							
XX	XX	(ALKE-) ALKERMES INC.							
XX	XX	Friden PM;							
XX	XX	WPI; 1993-196742/24.							
XX	XX	N-PSDB; AAQ43846.							
PT	PT	Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.							
XX	XX	Disclosure; Fig 17J; 151pp; English.							
XX	XX	The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAQ4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated.							

CC 128.1 is an anti-human transferrin receptor antibody which binds to the  
CC transferrin receptor on brain capillary endothelial cells. This antibody  
CC may be used in a conjugate in which it is linked to a neuropharmaceutical  
CC or diagnostic agent. The conjugate may be used to treat or prevent  
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 109 AA;  
  
Query Match 98.6%; Score 572; DB 2; Length 109;  
Best Local Similarity 98.2%; Pred. No. 1.6e-50;  
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
  
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109  
DB 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTSKTK 109  
  
RESULT 2  
AAV54997  
ID AAV54997 standard; protein; 109 AA.  
XX  
AC AAV54997;  
XX  
DT 17-FEB-2000 (first entry)  
DE Mutated CH2 sequence G2delta.  
XX  
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;  
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
KW sickle cell anaemia; coronary artery occlusion.  
XX  
OS Synthetic.  
XX  
PN WO9558572-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001441.  
PR 08-MAY-1998; 98GB-00009951.  
XX  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX  
PI Armour KL, Clark MR, Williamson LM;  
XX  
DR WPI; 2000-039075/03.  
XX  
PT Immunoglobulin-derived binding molecules that do not activate complement  
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin  
PT properties.  
XX  
PS Claim 12; Fig 17; 81pp; English.  
XX  
CC This sequence represents the mutated CH2 molecule G2delta, and is a  
CC binding molecule of the invention. The recombinant binding molecule is  
CC capable of binding a target molecule without triggering complement  
CC dependent lysis, or the cell-mediated destruction of the target  
CC comprises: (a) a binding domain capable of binding a target molecule; and  
CC (b) an effector domain that is homologous to all or part of a constant  
CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
CC molecule is used to bind a target molecule (especially FcgammaRIIb

CC causing inhibition of B cell activation, mast cell degranulation or  
CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
CC binding of a second binding molecule, e.g. an antibody, to the target  
CC molecule. The binding molecule is useful for the treatment of graft-vs-  
CC host disease, organ transplant rejection, bone-marrow transplant  
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.  
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
CC coronary artery occlusion). The binding molecules do not activate  
CC complement or trigger cytotoxic activities through FcgammaRIIb and desirable  
CC IgG properties have been retained. The polypeptides do not contain non-  
CC human amino acids, and are therefore likely to have reduced  
CC immunogenicity. Further, they still bind Protein A, which is consistent  
CC with being able to cross the human placenta through interaction with FcRn  
CC (neonatal Fc receptor)  
XX  
SQ Sequence 109 AA;  
  
Query Match 98.6%; Score 572; DB 3; Length 109;  
Best Local Similarity 99.1%; Pred. No. 1.6e-50;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
DB 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60  
  
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109  
DB 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109  
  
RESULT 3  
AAV54996  
ID AAV54996 standard; protein; 109 AA.  
XX  
AC AAV54996;  
XX  
DT 17-FEB-2000 (first entry)  
DE Mutated CH2 sequence G1deltaab.  
XX  
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;  
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
KW sickle cell anaemia; coronary artery occlusion.  
XX  
OS Synthetic.  
XX  
PN WO9558572-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001441.  
PR 08-MAY-1998; 98GB-00009951.  
XX  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX  
PI Armour KL, Clark MR, Williamson LM;  
XX  
DR WPI; 2000-039075/03.  
XX  
PT Immunoglobulin-derived binding molecules that do not activate complement  
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin  
PT properties.  
XX



```

PS  Claim 12; Fig 17; 81pp; English.
XX
XX  This sequence represents the mutated CH2 molecule G1deltaab, and is a
CC  binding molecule of the invention. The recombinant binding molecule is
CC  capable of binding a target molecule without triggering complement
CC  dependent lysis, or the cell-mediated destruction of the target
CC  comprises: (a) a binding domain capable of binding a target molecule; and
CC  (b) an effector domain that is homologous to all or part of a constant
CC  domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC  molecule is used to bind a target molecule (especially FcgammaRIIb
CC  causing inhibition of B cell activation, mast cell degranulation or
CC  phagocytosis). The binding molecule can be used to prevent or inhibit the
CC  binding of a second binding molecule, e.g. an antibody, to the target
CC  molecule. The binding molecule is useful for the treatment of graft-vs-
CC  host disease, organ transplant rejection, bone-marrow transplant
CC  rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC  autoimmune thrombocytopaenia and arthritis), autoimmunity (e.g.
CC  foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy),
CC  chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC  (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC  coronary artery occlusion). The binding molecules do not activate
CC  complement or trigger cytotoxic activities through FcgammaR and desirable
CC  IgG properties have been retained. The polypeptides do not contain non-
CC  human amino acids, and are therefore likely to have reduced
CC  immunogenicity. Further, they still bind Protein A, which is consistent
CC  with being able to cross the human placenta through interaction with FcRn
CC  (neonatal Fc receptor)
XX
SQ  Sequence 109 AA;
Query Match          96.9%; Score 562; DB 3; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.7e-49;
Matches 104; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY  1 APPVAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
DB  1 APPVAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
QY  61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
DB  61 REEQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKGLPSSIEKTSKAK 109
RESULT 4
ID  AAY54998 standard; protein; 110 AA.
XX
XX  AAY54998;
XX
XX  17-FEB-2000 (first entry)
XX
XX  Mutated CH2 sequence G1deltaac.
XX
XX  Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
KW  cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW  B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW  Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW  bone-marrow transplant rejection; autoimmunity disease; asthma; allergy;
KW  autoimmune disorder; autoimmunity haemolytic anaemia; inflammatory disease;
KW  autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis;
KW  neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy;
KW  sickle cell anaemia; coronary artery occlusion.
XX
XX  Synthetic.
XX
XX  WO9958572-A1.
XX
XX  18-NOV-1999.
XX
XX  07-MAY-1999; 99WO-GB001441.
XX
XX  08-MAY-1998; 98GB-00009951.
XX
XX

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PA  (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX  Armour KL, Clark MR, Williamson LM;
XX
XX  WPI; 2000-039075/03.
XX
XX  Immunoglobulin-derived binding molecules that do not activate complement
PT  or trigger cytotoxic activities and maintaining desirable immunoglobulin
PT  properties.
XX
XX  Claim 12; Fig 17; 81pp; English.
XX
XX  This sequence represents the mutated CH2 molecule G1deltaac, and is a
CC  binding molecule of the invention. The recombinant binding molecule is
CC  capable of binding a target molecule without triggering complement
CC  dependent lysis, or the cell-mediated destruction of the target
CC  comprises: (a) a binding domain capable of binding a target molecule; and
CC  (b) an effector domain that is homologous to all or part of a constant
CC  domain of a human immunoglobulin G (IgG) heavy chain. The binding
CC  molecule is used to bind a target molecule (especially FcgammaRIIb
CC  causing inhibition of B cell activation, mast cell degranulation or
CC  phagocytosis). The binding molecule can be used to prevent or inhibit the
CC  binding of a second binding molecule, e.g. an antibody, to the target
CC  molecule. The binding molecule is useful for the treatment of graft-vs-
CC  host disease, organ transplant rejection, bone-marrow transplant
CC  rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
CC  autoimmune thrombocytopaenia and arthritis), autoimmunity (e.g.
CC  foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy),
CC  chronic or acute inflammatory diseases (e.g. Crohn's, HDN
CC  (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
CC  coronary artery occlusion). The binding molecules do not activate
CC  complement or trigger cytotoxic activities through FcgammaR and desirable
CC  IgG properties have been retained. The polypeptides do not contain non-
CC  human amino acids, and are therefore likely to have reduced
CC  immunogenicity. Further, they still bind Protein A, which is consistent
CC  with being able to cross the human placenta through interaction with FcRn
CC  (neonatal Fc receptor)
XX
SQ  Sequence 110 AA;
Query Match          93.2%; Score 540.5; DB 3; Length 110;
Best Local Similarity 93.6%; Pred. No. 2.7e-47;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
QY  1 APPVA-GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
DB  1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 60
QY  60 PREQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
DB  61 PREQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
RESULT 5
AAR67438
ID  AAR67438 standard; protein; 109 AA.
XX
XX  AAR67438;
XX
XX  25-MAR-2003 (revised)
DT  08-JUL-1995 (first entry)
XX
XX  OKT3 monoclonal antibody fragment.
XX
XX  OKT3; monoclonal antibody; antibody engineering; immunosuppressive;
KW  humanized antibody.
XX
XX  Mus musculus.
XX
XX  WO9428027-A1.
XX
XX  PN
XX  PD
XX  PR
XX  08-DEC-1994.
XX

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PF 01-JUN-1994; 94WO-US006198.
XX
PR 01-JUN-1993; 93US-00070116.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Bluestone JA, Zivin RA, Jolliffe L;
XX
XX WPI; 1995-022721/03.
XX
XX P-PSDB; AAQ75356.
XX
XX New humanised OKT3 antibody with mutated Fc receptor binding region -
XX
XX PT useful as immunosuppressant to reduce transplant rejection, lacks the T-
XX
XX cell activating side effects of wild type antibody.
XX
XX PS Disclosure; Page 82-87; 135pp; English.
XX
XX The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-
XX
XX cell activating and immunosuppressive activity, and is used to treat
XX
XX CC transplant patients to prevent rejection. The antibody can be engineered
XX
XX CC to contain a human Fc region. By transferring the binding specificity
XX
XX CC into a human framework, the immunogenicity is reduced without affecting
XX
XX CC the immunosuppressive activity. (Updated on 25-MAR-2003 to correct FN
XX
XX CC field.)
XX
XX SQ Sequence 109 AA;
Query Match 92.4%; Score 536; DB 2; Length 109;
Best Local Similarity 94.3%; Pred. No. 7.6e-47;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 4 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
QY 64 QFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAK 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 6
AAR41717
ID AAR41717 standard; protein; 110 AA.
XX
XX AAR41717;
XX
AC AC
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX
XX Undefined ORF2 encoded by plasmid pAH4808.
XX
XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
XX
XX KW light; chain; variable; constant; region; anti-human; pAH4807;
XX
XX KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
XX
XX KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
XX
XX KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
XX
XX KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
XX OS Synthetic.
XX
XX WO9310819-A1.
XX
XX 10-JUN-1993.
XX
XX 24-NOV-1992; 92WO-US010206.
XX
XX 26-NOV-1991; 91US-00800458.
XX
XX (ALKE-) ALKERMES INC.
XX
XX Friden PM;
XX
XX WPI; 1993-196742/24.
XX
DR 01-JUN-1994; 94WO-US006198.
XX
XX N-PSDB; AAQ43848.
XX
XX Antibody conjugates specific for transferrin receptor - used for
XX
XX PT diagnosis and treatment of cancer, AIDS and neurological disorders.
XX
XX PS Disclosure; Fig 19J; 151pp; English.
XX
XX The sequences given in AAR41715-18 are encoded by the expression vector
XX
XX pAH4808. This vector represents the cloning of the human gamma isotype,
XX
XX CC gamma-4, with the variable region of the murine monoclonal antibody
XX
XX CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the
XX
XX CC heavy chain (VH) is derived from a murine source and the sequences
XX
XX CC encoding CH1, CH2 and CH3 are derived from a human source. This vector,
XX
XX CC in combination with the chimeric light chain vector, pAG4611 (see also
XX
XX CC AAQ43845), was transfected into SP2/0 cells and clones were isolated
XX
XX CC 128.1 is an anti-human transferrin receptor antibody which binds to the
XX
XX CC transferrin receptor on brain capillary endothelial cells. This antibody
XX
XX CC may be used in a conjugate in which it is linked to a neuropharmaceutical
XX
XX CC or diagnostic agent. The conjugate may be used to treat or prevent
XX
XX CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
XX
XX CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
XX
XX CC methods. (Updated on 25-MAR-2003 to correct FN field.)
XX
XX SQ Sequence 110 AA;
Query Match 92.4%; Score 536; DB 2; Length 110;
Best Local Similarity 94.3%; Pred. No. 7.7e-47;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 5 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 64
QY 64 QFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAK 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 7
ADD25659
ID ADD25659 standard; protein; 109 AA.
XX
XX AC ADD25659;
XX
XX 15-JAN-2004 (first entry)
XX
XX Binding domain-immunoglobulin fusion protein-associated protein #107.
XX
XX Binding domain; immunoglobulin; fusion protein; cytostatic;
XX
XX KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
XX
XX KW neuroprotective; hinge region; immunoglobulin heavy chain;
XX
XX KW CH2 constant region; CH3 constant region; IgG1;
XX
XX KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
XX
XX KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
XX
XX KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX
XX KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
XX OS Unidentified.
XX
XX US2003118592-A1.
XX
XX 26-JUN-2003.
XX
XX 25-JUL-2002; 2002US-00207655.
XX
XX 17-JAN-2001; 2001US-0367358P.
XX
XX 17-JAN-2002; 2002US-00053530.
XX
XX 03-JUN-2002; 2002US-0385691P.
XX
XX (GENE-) GENE-CRAFT INC.
XX
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX

```

DR WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a

PT subject having or suspected of having a malignant condition or a B-cell

PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

XX

XX Disclosure; SEQ ID NO 220; 157pp; English.

PS

CC The invention relates to a binding domain-immunoglobulin fusion protein

CC comprising a binding domain polypeptide that is fused to an

CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain

CC CH2 constant region polypeptide that is fused to the hinge region

CC polypeptide, and an immunoglobulin heavy chain CH3 constant region

CC polypeptide that is fused to the CH2 constant region polypeptide. The

CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin

CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge

CC region polypeptide, derived from (a) having 3 or more cysteine residues;

CC where the mutated human IgG1 immunoglobulin hinge region polypeptide

CC contains 2 cysteine residues, where the first cysteine is not mutated; a

CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from

CC (a) having 3 or more cysteine residues, where the mutated human IgG1

CC immunoglobulin hinge region polypeptide contains no more than one

CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region

CC polypeptide, derived from (a) having 3 or more cysteine residues; where

CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains

CC no cysteine residues. The binding domain-immunoglobulin fusion protein is

CC capable of at least one immunological activity comprising antibody

CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The

CC binding domain polypeptide is capable of specifically binding to an

CC antigen. Also included are an isolated polynucleotide encoding the

CC binding domain-immunoglobulin fusion protein, a recombinant expression

CC construct comprising the polynucleotide (operably linked to a promoter),

CC a host cell transformed or transfected with a recombinant expression

CC construct, producing the binding domain-immunoglobulin fusion protein, a

CC pharmaceutical composition comprising the binding domain-immunoglobulin

CC fusion protein or polynucleotide and a carrier, and treating a subject

CC having or suspected of having a malignant condition or a B-cell disorder.

CC The binding domain-immunoglobulin fusion protein is useful for treating a

CC subject having or suspected of having a malignant condition or a B-cell

CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,

CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple

CC sclerosis or autoimmune disease. The present sequence is a binding domain

CC immunoglobulin fusion protein-associated protein sequence. Note: The

CC sequence data for this patent formed part of the printed specification

CC and is also available in electronic format directly from USPTO at

CC [seqdata.uspto.gov/sequence.html?docID=20030118592](http://seqdata.uspto.gov/sequence.html?docID=20030118592). The authors have not

CC identified the sequences in the printed specification by their SEQ ID

CC number therefore none of the sequences can be explicitly identified.

XX

SQ Sequence 109 AA;

Query Match 90.2%; Score 523; DB 7; Length 109;

Best Local Similarity 90.6%; Pred. No. 1.6e-45;

Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQNMWYDGVGVEHNAKTKPREE 63

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 4 LGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQNMWYDGVGVEHNAKTKPREE 63

Qy 64 QFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 64 QYNSTYRWVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAK 110

RESULT 8

AAR27680

ID AAR27680 standard; protein; 110 AA.

XX

XX AAR27680;

XX

XX 25-MAR-2003 (revised)

DT 10-MAR-1993 (first entry)

XX

DE Human immunoglobulin IgG1 CH2 region.

XX

KW Isoallotype; IgG1 Glm(1,2,17); anti-allotype response; humanised Ab.

XX

OS Homo sapiens.

XX

PN WO9216562-A1.

XX

XX 01-OCT-1992.

PD

XX 12-MAR-1992; 92WO-GB000445.

PF

XX 12-MAR-1991; 91GB-00005245.

PR

XX (LYNX-) LYNXVALE LTD.

PA

XX Clark MR;

PI

XX WPI; 1992-349162/42.

DR

XX Humanised antibodies having modified allotypic determinant - useful for

PT matching allotypes in therapy with decreased likelihood of causing

PT undesirable immune responses.

PT

XX Disclosure; Fig 4c; 57pp; English.

PS

XX In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17.

CC The inventor's propose eliminating these allotypes by amino acid changes

CC to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype

CC sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes"

CC should be suitable for therapeutic use in all patients. See AAR27678-

CC R27681. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 110 AA;

Query Match 90.2%; Score 523; DB 2; Length 110;

Best Local Similarity 90.6%; Pred. No. 1.6e-45;

Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQNMWYDGVGVEHNAKTKPREE 63

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 5 LGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQNMWYDGVGVEHNAKTKPREE 64

Qy 64 QFNSTFRVSVLTIVVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 65 QYNSTYRWVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAK 110

RESULT 9

AAR41684

ID AAR41684 standard; protein; 110 AA.

XX

XX AAR41684;

XX

XX 25-MAR-2003 (revised)

DT 20-OCT-1993 (first entry)

XX

XX Undefined ORF2 encoded by pAH4602.

XX

XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;

KW Chain; variable; constant; region; anti-human; transferrin; receptor;

KW antibody; brain; capillary; endothelial cell; conjugate;

KW neuropharmacological; diagnostic; agent; tumour; AIDS; stroke; epilepsy;

KW Parkinsons disease; Alzheimers disease.

XX

XX Synthetic.

XX

XX WO9310819-A1.

PN

XX 10-JUN-1993.

PD

XX 24-NOV-1992; 92WO-US010206.

PF

XX

PR 26-NOV-1991; 91US-00800458.  
 XX (ALKE-) ALKERMES INC.  
 XX  
 XX Friden PM;  
 XX  
 XX WPI; 1993-196742/24.  
 DR N-PSDB; AAQ43844.  
 XX  
 XX Antibody conjugates specific for transferrin receptor - used for  
 PT diagnosis and treatment of cancer, AIDS and neurological disorders.  
 XX  
 XX Disclosure; Fig 11K; 151pp; English.  
 XX  
 XX The sequences given in AA41582-85 are encoded by the expression vector,  
 CC pAH4602. This vector contains open reading frames encoding the heavy  
 CC chain variable region (VH) of the antibody 128.1, an ampicillin  
 CC resistance gene and a histidine (histidinol) selection marker.  
 CC Transcription of the VH gene is from the VH promoter of the murine 27.44  
 CC gene. The vector also includes a heavy chain immunoglobulin enhancer and  
 CC the human gamma constant region (CH). The VH region of 128.1 was  
 CC isolated by polymerase chain reaction and cloned into plasmid pAH4274.  
 CC This was achieved by digesting the plasmid and the product with EcoRV and  
 CC NheI. The VH gene was inserted in-frame with the human gamma1 CH region  
 CC CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an  
 CC anti-human transferrin receptor antibody which binds to the transferrin  
 CC receptor on brain capillary endothelial cells. This antibody may be used  
 CC in a conjugate in which it is linked to a neuro- pharmaceutical or  
 CC diagnostic agent. The conjugate may be used to treat or prevent  
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 110 AA;

Query Match 90.2%; Score 523; DB 2; Length 110;  
 Best Local Similarity 90.6%; Pred. No. 1.6e-45;  
 Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 Qy 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 63  
 Db : |||||  
 5 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 64  
 Qy 64 QFNSTFRVSVLTIVHVDWLNKGKEYCKVSNKGLPSSIEKTSKTK 109  
 Db : |||||  
 65 QYNSTYRVSVLTIVLHQDWLNKGKEYCKVSNKALPAPIEKTISKAK 110

RESULT 10  
 ID ADH75385  
 XX ADH75385 standard; protein; 110 AA.  
 XX  
 XX ADH75385;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Human IgG1 CH2 region.  
 XX  
 XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
 KW autoimmune disease; human; IgG; immunoglobulin.  
 KW  
 XX Homo sapiens.  
 XX  
 XX US2004002587-A1.  
 PN  
 XX  
 PD 01-JAN-2004.  
 XX  
 XX 20-FEB-2003; 2003US-00370749.  
 PF  
 XX  
 PR 20-FEB-2002; 2002US-0358161P.  
 XX  
 XX (WATK/) WATKINS J D.  
 PA (ALLA/) ALLAN B.  
 XX

XX  
 PI  
 XX  
 XX Watkins JD, Allan B;  
 DR WPI; 2004-070755/07.  
 XX  
 XX New composition comprising a variant of a parent polypeptide having at  
 PT least a portion of a Fe region, useful in treating e.g., autoimmune  
 PT diseases.  
 XX  
 XX Claim 20; SEQ ID NO 23; 62pp; English.  
 XX  
 XX The invention relates to a new composition comprises a variant of a  
 CC parent polypeptide having at least a portion of a Fc region. The variant  
 CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the  
 CC presence of effector cells more effectively than the parent polypeptide  
 CC and comprises at least one amino acid modification at position 280 in the  
 CC Fc region. The composition is useful in treating diseases e.g.,  
 CC autoimmune diseases. The present sequence represents the amino acid  
 CC sequence of a human immunoglobulin G, IgG, CH region.  
 XX  
 XX Sequence 110 AA;

Query Match 90.2%; Score 523; DB 9; Length 110;  
 Best Local Similarity 90.6%; Pred. No. 1.6e-45;  
 Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 Qy 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNAKTPREE 63  
 Db : |||||  
 5 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREE 64  
 Qy 64 QFNSTFRVSVLTIVHVDWLNKGKEYCKVSNKGLPSSIEKTSKTK 109  
 Db : |||||  
 65 QYNSTYRVSVLTIVLHQDWLNKGKEYCKVSNKALPAPIEKTISKAK 110

RESULT 11  
 ID ADJ52132  
 XX ADJ52132 standard; protein; 102 AA.  
 XX  
 XX ADJ52132;  
 XX  
 XX 06-MAY-2004 (first entry)  
 DT  
 XX  
 XX CH1 deleted mimetibody-related CH2 peptide SeqID1124.  
 XX  
 XX CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;  
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;  
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;  
 KW anti-allergic; muscular-Gen; cytostatic; anti-inflammatory; neuroleptic;  
 KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;  
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;  
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;  
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;  
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;  
 KW obstetric disorder; haematologic disorder; immunologic disorder;  
 KW allergic disorder; infectious disorder; musculoskeletal disorder;  
 KW oncological disorder; neurological disorder; nutritional disorder;  
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;  
 KW renal disorder; pulmonary disorder.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX WO2004002424-A2.  
 PN  
 XX  
 XX 08-JAN-2004.  
 PD  
 XX  
 XX 30-JUN-2003; 2003WO-US020495.  
 PF  
 XX  
 XX 28-JUN-2002; 2002US-0392431P.  
 PR  
 XX 19-SEP-2002; 2002US-0412144P.  
 XX  
 XX (CENZ ) CENTOCOR INC.  
 XX

PI Heavner GA, Knight DM, Chrayeb J, Scallion BJ, Neespor TC;  
 XX Kutoloski KA;  
 DR WPI; 2004-082872/08.  
 XX  
 XX New CH1 deleted mimetibody polypeptide and nucleic acid, useful for  
 PT diagnosing, preventing or treating cardiovascular, dermatologic, and  
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic, and  
 PT nutritional disorders.  
 XX  
 XX Claim 7; SEQ ID NO 1124; 123pp; English.  
 PS  
 XX This invention relates to CH1 deleted mimetibodies (and the DNA sequences  
 CC which encode them), compositions, methods and uses. The invention may be  
 CC useful for the development of compounds with an osteopathic,  
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,  
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,  
 CC immunomodulator, anti-allergic, muscular-Gen, cytostatic,  
 CC anti-inflammatory, neuroleptic, ophthalmological, nephrotropic or  
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-  
 CC modulator or cytokine-agonist. The methods and compositions of the  
 CC present invention are useful for the diagnosis, prevention and/or  
 CC treatment of diseases or conditions associated with aberrant expression  
 CC or activity of the CH1 deleted mimetibody, such as a bone or joint,  
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,  
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,  
 CC obstetric, haematologic, immunological, allergic, infectious,  
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,  
 CC pediatric, psychiatric, renal or pulmonary disorders. The present  
 CC sequence is that of a CH2 peptide which may be used during the creation  
 CC of a mimetibody peptide of the invention.  
 XX  
 XX Sequence 102 AA;  
 SQ  
 Query Match 90.0%; Score 522; DB 8; Length 102;  
 Best Local Similarity 96.1%; Pred. No. 1.9e-45;  
 Matches 98; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 SVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNATKPREQFNS 67  
 DB 1 SVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNATKPREQFNS 60  
 QY 68 TFRVSVSLTVHVDWLNKGKCKVSNKGLPSSIEKTIKTK 109  
 DB 61 TYRVSLSLTVHVDWLNKGKCKVSNKGLPSSIEKTIKTK 102  
 RESULT 12  
 AAY42626  
 ID AAY42626 standard; protein; 105 AA.  
 XX  
 AC AAY42626;  
 XX  
 XX 10-JAN-2000 (first entry)  
 DT  
 XX Human IgG1 Fc gamma2 residues.  
 DE  
 XX Immunoglobulin E; IgE; antagonist; Fc epsilon RI receptor; human; bds;  
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;  
 KW allergic disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US5965709-A.  
 PN  
 XX 12-OCT-1999.  
 PD  
 XX 21-APR-1994; 94US-00232539.  
 PF  
 XX 14-AUG-1991; 91US-00744768.  
 PR  
 XX 07-JAN-1994; 94US-00178583.  
 XX  
 XX (GETH ) GENENTECH INC.

XX Jardieu PM, Presta LG;  
 PI WPI; 1999-579941/49.  
 XX  
 XX Immunoglobulin E variants as peptide antagonists useful for raising and  
 PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and  
 PT purification of Fc epsilon RI receptor and in the treatment of allergic  
 PT diseases.  
 XX  
 XX Claim 7; Col 63-64; 37pp; English.  
 PS  
 XX The invention provides immunoglobulin E (IgE) antagonists comprising one  
 CC or more of the Fc epsilon RI receptor-binding determinant sites of human  
 CC IgE. The antagonists include IgE variants comprising an immunoglobulin  
 CC template and binding determinant sequences (bds) CDBds, EFBds and the  
 CC sequence shown in AAY42581. The CDBds (CD loop binding determinant  
 CC sequence) are selected from the sequences shown in AAY42567-Y42577 and  
 CC the EFBds (EF loop binding determinant sequence) are selected from  
 CC sequences shown in AAY42578-Y42580. The variants are useful in raising  
 CC and screening anti-IgE antibodies, in the isolation and purification of  
 CC Fc epsilon RI receptor and in the treatment and prophylaxis of allergic  
 CC diseases  
 XX  
 XX Sequence 105 AA;  
 SQ  
 Query Match 90.0%; Score 522; DB 2; Length 105;  
 Best Local Similarity 92.3%; Pred. No. 1.9e-45;  
 Matches 96; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 GPSVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNATKPREQF 65  
 DB 1 GPSVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNATKPREQF 60  
 QY 66 NSTFRVSVSLTVHVDWLNKGKCKVSNKGLPSSIEKTIKTK 109  
 DB 61 NSTFRVSVSLTVHVDWLNKGKCKVSNKGLPSSIEKTIKTK 104  
 RESULT 13  
 AAE28089  
 ID AAE28089 standard; protein; 109 AA.  
 XX  
 AC AAE28089;  
 XX  
 DT 13-DEC-2002 (first entry)  
 DT  
 XX Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.  
 DE  
 XX Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;  
 KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;  
 KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;  
 KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;  
 KW virucide.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200260919-A2.  
 PN  
 XX 08-AUG-2002.  
 PD  
 XX 12-DEC-2001; 2001WO-US048432.  
 PF  
 XX 12-DEC-2000; 2000US-0254884P.  
 PR  
 XX 09-MAY-2001; 2001US-0289760P.  
 XX  
 XX (MEDI-) MEDIMUNE INC.  
 PA  
 XX Dall'acqua W, Johnson LS, Ward ES;  
 PI WPI; 2002-666925/71.  
 DR  
 XX Modified immunoglobulins useful in the treatment of autoimmune diseases,  
 PT

comprises at least one amino acid modification relative to a wild-type immunoglobulin constant domain.

Disclosure; Page 138; 147pp; English.

The invention relates to a modified immunoglobulin (IgG1) which comprises an IGG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-host, lymphoid malignancies and passive immunotherapies and also for the treatment of various systemic infections. The present sequence is human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain

Sequence 109 AA;

Query Match 89.3%; Score 518; DB 5; Length 109;  
Best Local Similarity 91.3%; Pred. NO. 5.2e-45;  
Matches 95; Conservative 6; Mismatches 3; Indels 0; Gaps 0

QY 4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVDSVSHEDPVEFNWYVDGVGHNAKTKPREE 63  
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 5 LGFSVFLFPPKPKDTLMISRTPEVTCVVDSVSHEDPVEFNWYVDGVGHNAKTKPREE 64  
:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 64 QFNSTFRVSVLTIVHQDLNGLKEYCKVSNKGLPSSIETISK 107  
:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 65 QYNSTRVWSVLTVLHQDLNGLKEYCKVSNKALPAIEKTISK 108  
:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14  
ADH75415  
ID ADH75415 standard; protein; 110 AA.  
XX  
AC ADH75415;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE CH2 region K290S variant.  
XX  
KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
KW autoimmune disease.  
XX  
OS Unidentified.  
XX  
PN US2004002587-A1.  
XX  
PD 01-JAN-2004.  
XX  
PF 20-FEB-2003; 2003US-00370749.  
XX  
PR 20-FEB-2002; 2002US-0358161P.  
XX  
PA (WATK/) WATKINS J D.  
PA (ALLA/) ALLAN B.  
XX  
PI Watkins JD, Allan B;  
XX  
DR WFI; 2004-070755/07.  
XX  
PT New composition comprising a variant of a parent polypeptide having at  
PT least a portion of a re region, useful in treating e.g., autoimmune  
PT diseases.  
XX  
PS Disclosure; SEQ ID NO 53; 62pp; English.  
XX  
CC The invention relates to a new composition comprises a variant of a  
CC parent polypeptide having at least a portion of a Fc region. The variant  
CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the  
CC presence of effector cells more effectively than the parent polypeptide  
CC and comprises at least one amino acid modification at position 280 in the  
CC Fc region. The composition is useful in treating diseases e.g.,  
CC autoimmune diseases. The present sequence represents a CH2 region

Qy	64 QFNSTFRWWSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTSKTK 109
Db	65 QYNSTYRWWSVLTVLHQDWLNGKEYKCKVFENKALPAPIEFTISKAK 110

Search completed: November 17, 2005, 07:47:00  
Job time : 90.0913 secs

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F;22-90/Domain: immunoglobulin homology <IMM>



```

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30554
J:Immunol. 142, 708-711, 1989
R:Foley, R.C.; Beh, K.J.
A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A:Reference number: A30554; MUID:89093962; PMID:2492052
A:Accession: B30554
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-105 <FOL>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:20-88/Domain: immunoglobulin homology <IMM>

Query Match 22.5%; Score 130.5; DB 2; Length 105;
Best Local Similarity 29.6%; Pred. No. 4e-06;
Matches 33; Conservative 23; Mismatches 46; Indels 7; Gaps 4;

Qy 3 PVAGPSVFLPPPKDITLMSRTPETVCVVVDVSHEDPEVQFNWYDGVH-NAKTKPR 61
Db ||| ||| ||| ||| : : : : : ||| ||| ||| ||| : : : |||
2 PKGAPSVTLFPSPKEE--LDTNKATVCLLSD--FYPGSVNVVKAOGSIINQNVKTQA 57
Qy 62 EEFNSNFRVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db ||| ||| ||| ||| ||| : : : : : ||| ||| ||| ||| : : : |||
58 SKOSNKYAASSVLTLTGSEWKSSTYCEVTHEG--STVTKTVKPS 103

RESULT 8
B26167
Ig lambda chain C region - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B26167
R:Parvari, R.; Ziv, E.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
A:Title: Analyses of chicken immunoglobulin light chain cDNA clones indicate a
A:Reference number: A26167; MUID:87218480; PMID:3107981
A:Accession: B26167
A:Molecule type: mRNA; DNA
A:Residues: 1-103 <PAR>
A:Cross-references: UNIPROT:P20763; GB:M33049
A:Note: 90-Asp was found in one cDNA clone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-87/Domain: immunoglobulin homology <IMM>

Query Match 22.1%; Score 128; DB 2; Length 103;
Best Local Similarity 29.0%; Pred. No. 7e-06;
Matches 31; Conservative 26; Mismatches 44; Indels 6; Gaps 5;

Qy 3 PVAGPSVFLPPPKDITLMSRTPETVCVVVDVSHEDPEVQFNWYDGVHNAKTKPRE 62
Db ||| ||| ||| ||| ||| : : : : : ||| ||| ||| ||| : : : |||
2 PKVAPTITLPPPS-KEELNATKATLVCLINDF-YPSF-VTVDWVIDG-STRSGETTPAQ 57
Qy 63 EQFNSTFRVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db ||| ||| ||| ||| ||| : : : : : ||| ||| ||| ||| : : : |||
58 RQNSQYMASSVLSLSADSWSSHETVTCRVTHNG--TSITKTLKRSE 102

RESULT 9
B26434
Ig lambda-5 chain C region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C:Accession: B26434
R:Sakaguchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A:Title: Lambda-5, a new light-chain-related locus selectively expressed in pre
A:Reference number: A26434; MUID:87065143; PMID:3024017
A:Accession: B26434
A:Molecule type: mRNA
A:Residues: 1-105 <SAK>

```



Biochemistry 14, 3953-3961, 1975  
A;Title: Rotational allomerism and divergent evolution of domains in immunoglobulin light chain C region - western wild mouse  
A;Reference number: A90391  
A;Contents: annotation; MCG; X-ray crystallography, 2.3 angstroms  
R;Hieter, P.A.; Hollis, G.F.; Korsmeyer, S.J.; Waldmann, T.A.; Leder, P.  
Nature 294, 536-540, 1981  
A;Title: Clustered arrangement of immunoglobulin lambda constant region genes in man.  
A;Reference number: A93268; MUID:8208680; PMID:6273747  
A;Accession: A93268  
A;Molecule type: DNA  
A;Residues: 1-105 <HE>  
A;Cross-references: GB:J00253; NID:G186118; PIDN:AAA59107.1; PID:G186127  
A;Note: six tandem lambda-type genes were identified and the three most 5' were sequenced (lambda-3)  
C;Comment: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins Sh, X, and N  
C;Genetics:  
A;Gene: GDB:IGLC2; IGLC  
A;Cross-references: GDB:120691; OMIM:147220  
A;Map position: 22q11.2-22q11.2  
C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotrimer  
F;20-88/Domain: immunoglobulin homology <IMM>  
F;27-86/Disulfide bonds: #status experimental  
F;104/Disulfide bonds: interchain (to heavy chain) #status experimental  
Query Match 20.8%; Score 120.5; DB 1; Length 105;  
Best Local Similarity 27.8%; Pred. No. 4.1e-05;  
Matches 30; Conservative 25; Mismatches 46; Indels 7; Gaps 4;  
Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61  
Db 2 PKAASVTLPPPSSEEL---LQAKATLVCLISD--FYFGAVTVAKADSSPVKAGVETTP 57  
Qy 62 EEQFNSTFRVSVLTVVHQDNLNGKEYCKVSKNGLPSSIEKTKIS 109  
Db 58 SKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEG--STVEKTVAPTE 103  
RESULT 12  
S22760  
Ig lambda-2 chain C region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: S22760  
R;Weiss, S.; Wu, G.E.  
EMBO J. 6, 927-932, 1987  
A;Title: Somatic point mutations in unrearranged immunoglobulin gene segments encoding the C region of the lambda-2 chain of the mouse (fragment)  
A;Reference number: S22759; MUID:87246527; PMID:3109891  
A;Accession: S22760  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-106 <WEI>  
A;Cross-references: UNIPROT:Q9D8W4; EMBL:X58411; NID:G51763; PIDN:CAA41312.1; PID:G51764  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;21-89/Domain: immunoglobulin homology <IMM>  
Query Match 20.8%; Score 120.5; DB 2; Length 106;  
Best Local Similarity 29.2%; Pred. No. 4.1e-05;  
Matches 31; Conservative 20; Mismatches 48; Indels 7; Gaps 3;  
Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61  
Db 3 PKSSPSVTLPPPSSEEL---ETNKATLVCTITDFYFGVTVVQDKVDGTPVQGMETTP 58  
Qy 62 EEQFNSTFRVSVLTVVHQDNLNGKEYCKVSKNGLPSSIEKTKIS 107  
Db 59 SKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEG--HTVEKSLSR 102  
RESULT 13

S00259  
Ig lambda-5 chain C region - western wild mouse  
C;Species: Mus spretus (western wild mouse)  
C;Date: 31-Dec-1988 #sequence\_revision 07-Sep-1990 #text\_change 21-Jan-2000  
C;Accession: S00259  
R;Mami, F.; Cazenave, P.A.; Kindt, T.J.  
EMBO J. 7, 117-122, 1988  
A;Title: Conservation of the immunoglobulin C-lambda-5 gene in the Mus genus.  
A;Reference number: S00259; MUID:88196070; PMID:3129289  
A;Accession: S00259  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-106 <MAM>  
A;Note: the sequence was translated from the germline gene  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;21-89/Domain: immunoglobulin homology <IMM>  
Query Match 20.6%; Score 119.5; DB 2; Length 106;  
Best Local Similarity 29.5%; Pred. No. 5.2e-05;  
Matches 31; Conservative 23; Mismatches 44; Indels 7; Gaps 3;  
Qy 3 PVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61  
Db 3 PKSDPLVTLPLPSLKNL----QANKVTLVCLVSEFPCTLVVDKVDGVPVQGVETTP 58  
Qy 62 EEQFNSTFRVSVLTVVHQDNLNGKEYCKVSKNGLPSSIEKTKIS 106  
Db 59 SKQTNKMYSSYLSLTISDQMPHSRYSCRVTHEG--NTVEKSVS 101  
RESULT 14  
B34509  
Ig light chain C region 3 - sandbar shark (fragment)  
C;Species: Carcharias plumbeus (sandbar shark)  
C;Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 17-Nov-2000  
C;Accession: B34509  
R;Schluter, S.F.; Hohman, V.S.; Edmundson, A.B.; Marchalonis, J.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989  
A;Title: Evolution of immunoglobulin light chains: cDNA clones specifying sandbar shark  
A;Reference number: A34509; MUID:90099382; PMID:2513577  
A;Accession: B34509  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-102 <SCH>  
A;Cross-references: GB:M29044; NID:G212941; PIDN:AAA49153.1; PID:G212942  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
Query Match 20.3%; Score 118; DB 2; Length 102;  
Best Local Similarity 32.6%; Pred. No. 7e-05;  
Matches 30; Conservative 17; Mismatches 41; Indels 4; Gaps 3;  
Qy 7 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDG-VEVHNAKTKPREOF 65  
Db 13 PSVSLPPSP-DOITAKNTATLVCLVSGFKPGAAEIE--WTVDGVRGNGVETSRVQEEA 69  
Qy 66 NSTFRVSVLTVVHQDNLNGKEYCKVSKNGL 97  
Db 70 DNTFVSYSYLTLSASDWSHLYSCLVKHEAL 101  
RESULT 15  
S26654  
Ig lambda chain C region - chimpanzee (fragment)  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
C;Accession: S26654  
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybridomas 1, 23-26, 1990  
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
A;Reference number: S26652; MUID:91355693; PMID:2129418  
A;Accession: S26654

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-98 <EHR>  
A;Cross-references: EMBL:X65286  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-88/Domain: immunoglobulin homology <IMM>

Query Match 19.7%; Score 114.5; DB 2; Length 98;  
Best Local Similarity 29.1%; Pred. No. 0.00015;  
Matches 30; Conservative 21; Mismatches 45; Indels 7; Gaps 4;

Qy 3 PVAGPSVFLPPKPKDTLMISRTEVTCVVVDVSHEDPEVQFNWYVDGVEVH-NAKTKPR 61  
Db 2 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYFGAVTVAWKADSSPVKAGVETTP 57

Qy 62 BEQFNSTFRVSVLTVVHQDLNKGKEYCKVSNKGLPSSIEKT 104  
Db 58 SKQSNKKYAAASSVLSLTPEQWKSHKSYSCQVTHEG--STVEKT 98

Search completed: November 17, 2005, 07:55:07  
Job time : 16.4247 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.1461 Seconds  
(without alignments)  
723.518 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIBKTSKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	135	23.3	106	1 KAC_HUMAN	P01834 homo sapien
2	128	22.1	103	1 LAC_CHICK	P20763 gallus gall
3	123.5	21.3	106	2 Q8TCJ5	Q8tcj5 homo sapien
4	120.5	20.8	105	1 LAC1_MOUSE	P01843 mus musculu
5	120.5	20.8	105	1 LAC1_HUMAN	P01842 homo sapien
6	119.5	20.6	105	1 LAC5_MUSP	P20765 mus spratus
7	115.5	19.9	105	1 LAC5_MOUSE	P20764 mus musculu
8	109.5	18.9	103	1 KAC4_RABIT	P01840 oryctolagus
9	104.5	18.0	105	1 LAC1_PIG	P01846 sus scrofa
10	102.5	17.7	105	1 LAC6_RABIT	P01847 oryctolagus
11	100	17.2	104	1 KAC5_RABIT	P01984 oryctolagus
12	100	17.2	104	1 LAC1_RAT	P20766 rattus norv
13	100	17.2	106	1 KAC_MOUSE	P01837 mus musculu
14	96	16.6	106	1 KACB_RABIT	P01839 oryctolagus
15	92	15.9	106	1 KACB_RAT	P01835 rattus norv
16	90	15.5	104	1 KAC9_RABIT	P01838 oryctolagus
17	90	15.5	103	1 LAC2_RAT	P20767 rattus norv
18	88	15.2	103	1 KAC5_RABIT	P01841 oryctolagus
19	87	15.0	106	1 KACA_RAT	P01836 rattus norv
20	86	14.8	104	1 LAC3_MOUSE	P01845 mus musculu
21	79	13.6	104	1 LAC2_MOUSE	P01844 mus musculu
22	79	13.6	105	2 Q99JC1	Q99jc1 mus musculu
23	67	11.6	107	2 Q8KY10	Q8ky10 bacillus an
24	67	11.6	107	2 Q6E215	Q6e215 bacillus an
25	65.5	11.3	74	2 P79659	P79659 oncorhynch
26	65.5	11.3	74	2 P79659	P79660 oncorhynch
27	63	10.9	91	2 Q31248	Q31248 peromyscus
28	62.5	10.8	104	2 Q30837	Q30837 ovis aries
29	62	10.7	79	1 SNRP_HUMAN	P80697 homo sapien
30	61	10.5	73	2 Q8FBV4	Q8fbv4 escherichia
31	61	10.5	93	2 Q6LBV9	Q6lbv9 mus musculu

RESULT 1  
KAC\_HUMAN  
ID KAC\_HUMAN STANDARD; PRT; 106 AA.  
AC P01834;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 23-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig kappa chain C region.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE (MYELOMA PROTEIN EU).  
RX MEDLINE=71064023; PubMed=5489770;  
RA Gattlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";  
RL Biochemistry 9:3155-3161(1970).  
RN [2]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [3]  
RP SEQUENCE (BENCE-JONES PROTEIN TI).  
RX MEDLINE=72188439; PubMed=5027703;  
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;  
RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;  
RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";  
RL Cell 22:197-207(1980).  
RN [5]  
RP SEQUENCE (BENCE-JONES PROTEIN ROY).  
RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
RA Steimetz-Kayne M., Suter L., Watanabe S.;  
RT (in) Franek F., Shugar D. (eds.);  
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).  
RN [6]  
RP SEQUENCE (BENCE-JONES PROTEIN CUM).  
RX MEDLINE=68242259; PubMed=5586923;  
RA Hilschmann N.;

ALIGNMENTS

32	60.5	10.4	74	2	P79661
33	60.5	10.4	93	2	Q6LBW2
34	60	10.3	102	2	Q8HB97
35	59.5	10.3	55	2	Q768W8
36	59.5	10.3	92	2	O41412
37	59	10.2	91	2	Q9JKP1
38	59	10.2	98	2	Q7XZF9
39	59	10.2	99	2	Q9DG61
40	59	10.2	100	2	Q649X2
41	59	10.2	106	2	Q31261
42	58.5	10.1	74	2	P79652
43	58.5	10.1	74	2	P79657
44	58.5	10.1	93	2	O19471
45	58.5	10.1	93	2	O19472

P79661	oncorhynchu
Q6lbw2	mus musculu
Q8hb97	podarcis hi
Q768w8	uncultured
O41412	human immun
Q9jkp1	marmota mon
Q7xzf9	oryza sativ
Q9dg61	salmo salar
Q649x2	uncultured
Q31261	rattus norv
P79652	oncorhynchu
P79657	oncorhynchu
O19471	mus musculu
O19472	mus musculu

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-  
 type).",  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [7]  
 RP SEQUENCE (BENCE-JONES PROTEIN AG).  
 RX MEDLINE=69234734; PubMed=4893682;  
 RA Titani K., Shinoda T., Putnam F.W.;  
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
 complete sequence and the location of the disulfide bridges.";  
 RL J. Biol. Chem. 244:3550-3560(1969).  
 RN [8]  
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).  
 RX MEDLINE=70201507; PubMed=5447531;  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy  
 chains".  
 RL Science 169:56-59(1970).  
 RN [9]  
 RP SEQUENCE OF 1-33; 38-41 AND 62-80.  
 RC TISSUE=Abdominal adipose tissue;  
 RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;  
 RA Olsen K.E., Sletten K., Westermarck P.;  
 RT "Extended analysis of AL-amyloid protein from abdominal wall  
 subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";  
 RL Biochem. Biophys. Res. Commun. 245:713-716(1998).  
 CC -!- MISCELLANEOUS: The EU sequence has the INV (3) allotypic marker,  
 Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic  
 marker, Ala-45 and Leu-83.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; J00241; AAA59899.1; -.  
 DR PIR; B90562; K3HU.  
 DR PDB; 1D5B; X-ray; A/L=1-103.  
 DR PDB; 1D5I; X-ray; L=1-103.  
 DR PDB; 1D6V; X-ray; L=1-103.  
 DR PDB; 1HEZ; X-ray; -.  
 DR PDB; 1HKL; X-ray; L=1-106.  
 DR PDB; 1I72; X-ray; A/C=1-106.  
 DR PDB; 1MIM; X-ray; L=1-105.  
 DR Genew; HGNC:5716; IGKC.  
 DR H-invDB; HIX0021121; -.  
 DR MIM; 147200; -.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR 3D-structure; Direct protein sequencing; Immunoglobulin C region;  
 Immunoglobulin domain.  
 KW NON\_TER 1 1  
 KW DOMAIN 5 102 Ig-like.  
 FT DISULFID 26 86  
 FT DISULFID 106 106 Interchain (with a heavy chain).  
 FT VARIANT 83 83 V -> L (in INV(1,2) marker).  
 FT FTID=VAR\_003897.  
 FT CONFLICT 14 14 D -> N (in Ref. 7 and 8).  
 FT CONFLICT 57 57 E -> Q (in Ref. 5 and 6).  
 FT STRAND 3 3  
 FT STRAND 6 10  
 FT HELIX 14 17  
 FT TURN 18 20  
 FT STRAND 21 32  
 FT STRAND 37 42

FT TURN 43 44  
 FT STRAND 45 47  
 FT STRAND 51 55  
 FT TURN 60 62  
 FT STRAND 65 74  
 FT HELIX 75 79  
 FT TURN 80 80  
 FT STRAND 83 89  
 FT TURN 91 92  
 FT STRAND 97 102  
 FT TURN 103 104  
 SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;  
 Query Match 23.1%; Score 135; DB 1; Length 106;  
 Best Local Similarity 31.1%; Pred. No. 9.5e-06;  
 Matches 33; Conservative 26; Mismatches 41; Indels 6; Gaps 3;  
 QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCTVVVDVSHEDPEVQFNWYVDGV--EVHNAKTKPR 61  
 DB 2 VAAPSVFIPP--PSDQLKSGTASVCLLNFFPREAKVQ--WKVDNALQSGNSQESVTE 57  
 QY 62 EEQFNSTFRVSVLTVVHQDLNGKEYKCKVSNKGLPSSIEKTISK 107  
 DB 58 QDSKDSYLSLSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNR 103  
 RESULT 2  
 LAC\_CHICK  
 ID - LAC\_CHICK STANDARD; PRT; 103 AA.  
 AC P20763;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig lambda chain C region.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87218480; PubMed=3107981;  
 RA Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;  
 RT "Analyses of chicken immunoglobulin light chain cDNA clones indicate a  
 few germline V lambda genes and allotypes of the C lambda locus.";  
 RL EMBO J. 6:97-102(1987).  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X04768; CAA28461.1; -.  
 DR FIR; B26167; B26167.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin C region; Immunoglobulin domain; Polymorphism.  
 KW NON\_TER 1 1  
 KW DOMAIN 6 99 Ig-like.  
 FT DISULFID 28 85  
 FT DISULFID 103 103 Interchain (with heavy chain).  
 FT VARIANT 90 90 N -> D.  
 SQ SEQUENCE 103 AA; 11361 MW; 77BF341B511B91B2 CRC64;



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Query Match          22.1%; Score 128; DB 1; Length 103;
Best Local Similarity 29.0%; Pred. No. 4.6e-05;
Matches 31; Conservative 26; Mismatches 44; Indels 6; Gaps 5;

QY 3 PVAGPSVLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPR 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 PKVAPITLFPSPS-KEELNEATKATLVCLINDF-YPSF-VTVDWIDG-STRSGETTPAQ 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 EQFNSTFRVSVLTVVHVDWLNKGYKCKVSNKGLPSSIEKTIKTK 109
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 58 RQSNQYMASSVLSLSASDSSSHETTCRVTHNG--TSITKTLKRE 102
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
Q8TCJ5 PRELIMINARY; PRT; 106 AA.
AC Q8TCJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp667J0810 (Fragment).
GN Name=DKFZp667J0810;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -
DR HSP; P01842; LIL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 106 AA; 11265 MW; 145272BB65F4565 CRC64;

Query Match          21.3%; Score 123.5; DB 2; Length 106;
Best Local Similarity 28.7%; Pred. No. 0.00013;
Matches 31; Conservative 24; Mismatches 46; Indels 7; Gaps 4;

QY 3 PVAGPSVLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVH-NAKTKPR 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 PKAAPSVTLFPSSSE--LQNKATLVCLISD--FYQAVTVAVKASSPKAGVETTP 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 EQFNSTFRVSVLTVVHVDWLNKGYKCKVSNKGLPSSIEKTIKTK 109
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 59 SKQSNKYAASSVLSLTPEQMKSHKSYSCQVTHEG--STVEKTVAPTE 104
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
LAC1 MOUSE STANDARD; PRT; 105 AA.
ID LAC1 MOUSE
AC P01843;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; PubMed=6812053;
RA Seising E., Miller J., Wilson R., Storb U.;
RT "Evolution of mouse immunoglobulin lambda genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE=81148806; PubMed=6259534;
RA Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA Gefter M.L., Baltimore D.;
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL Nature 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE=82220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=71107854; PubMed=5276767;
RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
CC -1- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
CC normal lambda-2 chain and 1 abnormal lambda-1 chain that is
CC missing a large part of the V region. The C region sequence (shown
CC here) appears completely normal.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; J00582; AAA51636.1; -
DR EMBL; J00587; AAB59672.1; -
DR PIR; A93922; LIMS.
DR PDB; 1JNH; X-ray; A=1-105.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON TER 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
FT CONFLICT 19 20 ET -> TE (in Ref. 4).
FT CONFLICT 56 56 Q -> E (in Ref. 4).
FT CONFLICT 75 75 Missing (in Ref. 4).
FT CONFLICT 81 82 HS -> SH (in Ref. 4).
FT CONFLICT 85 85 S -> SS (in Ref. 4).
FT CONFLICT 96 96 E -> Q (in Ref. 4).
FT STRAND 4 4
FT STRAND 7 7
FT STRAND 10 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 22 33
FT STRAND 37 43
FT TURN 44 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 52 54
FT STRAND 58 60
FT TURN 61 63

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FT STRAND 64 74
FT HELIX 75 80
FT STRAND 84 90
FT TURN 91 92
FT STRAND 93 99
SQ SEQUENCE 105 AA; 11575 MW; A99F2B09BFCFA018 CRC64;

Query Match 20.8%; Score 120.5; DB 1; Length 105;
Best Local Similarity 29.2%; Pred. No. 0.00027;
Matches 31; Conservative 20; Mismatches 48; Indels 7; Gaps 3;

Qy 3 PVAGPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNYYVDGVEY-HNAKTKPR 61
Db 2 PKSPSPVTLFPSPSEEL-----ETNKATLVCTITDFYFGVVTVDWKVDGTPVTQGMETQP 57

Qy 62 EEOFNSTFRVSVLTVVHQDLNCKEYKCKVSNKGLPSSLEKTIISK 107
Db 58 SKQSNKYMSSYLTLTARAWERHSSYSCQVTHEG--HTVEKLSLR 101

RESULT 5
LAC_HUMAN STANDARD; PRT; 105 AA.
AC P01842; F80423;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda chain C regions.
GN Name=IGLC1;
GN and
GN Name=IGLC2;
GN and
GN Name=IGLC3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN SH).
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges."
RL J. Biol. Chem. 245:2171-2176 (1970).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX MEDLINE=69088380; PubMed=4883841;
RA Milstein C., Clegg J.B., Jarvis J.M.;
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT Bence-Jones protein."
RL Biochem. J. 110:631-652 (1968).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN NTG-64).
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup."
RL J. Biochem. 93:421-429 (1983).
RN [4]
RP SEQUENCE (BENCE-JONES PROTEIN KERN).
RX MEDLINE=71150336; PubMed=5549568;
RA Ponstingl H., Hess M., Hilschmann N.;
RT "Structural rule of antibodies. Primary structure of a monoclonal
RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT protein Kern). V. The complete amino acid sequence and its genetic
RT interpretation."
RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266 (1971).
RN [5]
RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX MEDLINE=74109253; PubMed=4814727;
RA Chen B.L., Poljak R.J.;

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RT "Amino acid sequence of the (lambda) light chain of a human myeloma
RT immunoglobulin (IG New)."
RL Biochemistry 13:1295-1302 (1974).
RN [6]
RP SEQUENCE (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins."
RL Eur. J. Biochem. 228:886-893 (1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX MEDLINE=75046825; PubMed=4215080;
RA Poljak R.J., Anzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA Saul F.;
RT "The three-dimensional structure of the fab' fragment of a human
RT myeloma immunoglobulin at 2.0-A resolution."
RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444 (1974).
RN [8]
RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX MEDLINE=75013804; PubMed=4415202;
RA Fetz J.W., Deutsche H.F.;
RT "Primary structure of the Mcg lambda chain."
RL Biochemistry 13:4102-4114 (1974).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RX Edmondson A.B., Ely K.R., Abola E.E., Schiffer M., Panagiotopoulos N.;
RT "Rotational allomerism and divergent evolution of domains in
RT immunoglobulin light chains."
RL Biochemistry 14:3953-3961 (1975).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MCG.
RX MEDLINE=90133913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harker M., Edmondson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
RT water. Conformational flexibility of a molecule in two crystal
RT forms."
RL J. Mol. Biol. 210:601-615 (1989).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=82080680; PubMed=6273747;
RA Hieter P.A., Hollis G.F., Korsmeyer S.J., Waidmann T.A., Leder P.;
RT "Clustered arrangement of immunoglobulin lambda constant region genes
RT in man."
RL Nature 294:536-540 (1981).
CC -!- MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg- chain
CC found in proteins SH, X, and NIG-84. The Kern protein has the
CC Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein
CC has the Kern+ marker, and the Mcg+ marker.
CC -!- MISCELLANEOUS: Six tandem lambda-type genes were identified and
CC the 3 most 5' were sequenced. These correspond to the Mcg sequence
CC (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz+
CC sequence (lambda-3).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00253; AAA59107.1; -
CC EMBL; L38582; AAB36581.1; ALT_INIT.
CC EMBL; X51754; CAB38569.1; ALT_INIT.
CC EMBL; X51755; CAA36049.1; -
CC EMBL; X51755; CAA36051.1; -
CC PIR; A92057; L2HU.
CC PDB; 1AOK; X-ray; L=1-105.
CC PDB; 1LIL; X-ray; A/B=1-105.
CC PDB; 2MCG; X-ray; -
CC PDB; 7FAB; X-ray; L=1-105.

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DR Genew; HGNC:5855; IGLC1.
DR Genew; HGNC:5856; IGLC2.
DR Genew; HGNC:5857; IGLC3.
DR H-InvDB; HIX0016285; -.
DR MIM; 147220; -.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0007110; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100
FT DISULFID 27 86
FT DISULFID 104 104
FT VARIANT 5 5
FT VARIANT 7 7
FT VARIANT 45 45
FT VARIANT 56 56
FT VARIANT 82 82
FT STRAND 8 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 24 32
FT STRAND 38 43
FT TURN 44 45
FT STRAND 46 48
FT STRAND 52 59
FT TURN 61 62
FT STRAND 65 72
FT HELIX 75 80
FT STRAND 84 89
FT STRAND 94 99
SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;

Query Match 20.8%; Score 120.5; DB 1; Length 105;
Best Local Similarity 27.8%; Pred. No. 0.00027;
Matches 30; Conservative 25; Mismatches 46; Indels 7; Gaps 4;

QY 3 PVAGPSVFLPPPKOTLMISRTPEVTCVVVDVSHEDPEVFQWVYDGVVH-NAKTKPR 61
DB 2 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYFGAVTVAKADSSPVKAGVETTP 57
QY 62 EEQPNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTK 109
DB 58 SKQSNKYAASSLSLTPQMKSHRSYSCQWTHG--STVEKTVAPTE 103

RESULT 6
LACS MUSSP
ID LACS MUSSP STANDARD; PRT; 105 AA.
AC P20765;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-5 chain C region.
OS Mus spretus (western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88196070; PubMed=3129289;
RA Mani F.; Cazenave P.A.; Kindt T.J.;
RT "Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
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EMBO J. 7:117-122(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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EMBL; M35582; AAA39152.1; -.
HSSP; P01843; LUNH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 1
FT DOMAIN 6 100
FT DISULFID 27 86
FT DISULFID 104 104
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11674 MW; AAB417DF68471A17 CRC64;

Query Match 20.6%; Score 119.5; DB 1; Length 105;
Best Local Similarity 29.5%; Pred. No. 0.00033;
Matches 31; Conservative 23; Mismatches 44; Indels 7; Gaps 3;

QY 3 PVAGPSVFLPPPKOTLMISRTPEVTCVVVDVSHEDPEVFQWVYDGVVH-NAKTKPR 61
DB 2 PKSDPLVTLFPLSLKNL---QANKVTLVCLSEFYPTGLVVDWKVDGVPVTCQGVETTP 57
QY 62 EEQPNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTK 106
DB 58 SKQTNKMYVSVSYLTLSIDQMPHRSYSCRTVTHG--NTVEKSVS 100

RESULT 7
LACS MOUSE
ID LACS MOUSE STANDARD; PRT; 105 AA.
AC P20764;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-5 chain C region.
GN Name=Igl-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87065143; PubMed=3024017;
RA Sakaguchi N., Melchers F.;
RT "Lambda 5, a new light-chain-related locus selectively expressed in
pre-B lymphocytes."
RL Nature 324:579-582(1986).
CC -!- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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EMBL; M30387; ; NOT_ANNOTATED_CDS.
DR HSSP; P01843; LUNH.
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DR MGD; MGI:96529; Igl-5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11678 MW; 1F210915904A86A5 CRC64;

Query Match 19.9%; Score 115.5; DB 1; Length 105;
Best Local Similarity 30.5%; Pred. No. 0.00084;
Matches 32; Conservative 25; Mismatches 41; Indels 7; Gaps 5;

QY 3 PVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV-HNAKTKPR 61
Db 2 PKSDPLVTLEPLSKN-LQPTR-PQLVCLVSE--FYPGTLVDWKVDGVPVQTGVETTPQ 57
QY 62 BEQENSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIIS 106
Db 58 SKOTNNKYMVSSYLTLLISDQMPHSRTSCRVTHEG--NTVEKSVS 100

RESULT 8
KAC4 RABIT
ID "KAC4_RABIT STANDARD; PRT; 103 AA.
AC P01840;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa-b4 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83300036; PubMed=6411231;
RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
RT allotype J-C locus and evidence for several b4-related sequences in
RT the rabbit genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a
RT kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.C.S., Kindt T.J., Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody
RT to streptococcal carbohydrate. II. Sequence determination of peptides
RT from tryptic and peptic digests.";
RL J. Biol. Chem. 250:3289-3296(1975).
CC -1- MISCELLANEOUS: This chain was obtained from antibody to the
CC specific carbohydrate of group C Streptococci and was isolated
CC from the serum of a single rabbit.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; X00231; CAA25051.1; -.
DR PIR; A93971; K4RB.
DR HSSP; P01837; ILCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 95 Ig-like.
FT DOMAIN 5 95
FT DISULFID 26 85 Interchain (with a heavy chain).
FT DISULFID 103 103 N -> D (in Ref. 3).
FT CONFLICT 58 58
SQ SEQUENCE 103 AA; 11043 MW; 5FCSACCB60E68DB CRC64;

Query Match 18.9%; Score 109.5; DB 1; Length 103;
Best Local Similarity 30.8%; Pred. No. 0.0033;
Matches 32; Conservative 20; Mismatches 39; Indels 13; Gaps 6;

QY 3 PVAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVE---VHNAKT 58
Db 2 PVA-PTVLIFPPAADQ--VATGTVITVCV---ANKYFPDVTVTWEVDGTTQTGTIENSKT 55
QY 59 KPREEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIE 102
Db 56 P--QNSADCTYNLSLTLTSTQYNSHKEYTCKVT-QGTTSVVQ 96

RESULT 9
LAC_PIG
ID "LAC_PIG STANDARD; PRT; 105 AA.
AC P01846;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=78000254; PubMed=409425;
RA Novotny J., Franek F., Margolies M.N., Haber E.;
RT "Amino acid sequence of normal (microheterogeneous) porcine
RT immunoglobulin lambda chains.";
RL Biochemistry 16:3765-3772(1977).
CC -1- MISCELLANEOUS: This chain was obtained from a mixture of normal
CC immunoglobulins.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02129; L1PG.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 100 Ig-like.
FT DOMAIN 2 100
FT DISULFID 27 86 Interchain (with heavy chain).
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11003 MW; 3817AAEBD747C396 CRC64;

Query Match 18.0%; Score 104.5; DB 1; Length 105;
Best Local Similarity 27.5%; Pred. No. 0.011;
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Matches 30; Conservative 21; Mismatches 49; Indels 9; Gaps 4;
Qy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNA--KTKP 60
Db 2 PKAAPTVNLPPPSSEEL---GTNKATLVCLISDFYPCGAVTVTWKAGTTVTQGVETTKP 57
Qy 61 REEQFNSTFRVSVLVTVVHQDWLNGKEYCKVKSNKGLPSSIEKTIKTK 109
Db 58 -SKOSNNKYAASSYLALASADWKSSSGFTQVTHEG--TIVEKTVTPSE 103

RESULT 10
LAC1_RABIT
ID -LAC1_RABIT STANDARD; PRT; 105 AA.
AC P01847;
DT 21-FEB-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=82091105; PubMed=6797414;
RA Garcia I., Jaton J.-C.;
RT "The primary structure of the constant region of Basilea-rabbit
RT immunoglobulin lambda-chains";
RL Biochem. J. 197;177-183(1981).
CC -I- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
CC specificity.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02130; L7RB.
DR HSSP; P01842; 1AOK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IGLIKE; 1.
DR PROSITE; PS00290; IGMHC; FALSE_NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON TER 1 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 17.7%; Score 102.5; DB 1; Length 105;
Best Local Similarity 25.7%; Pred. No. 0.017;
Matches 27; Conservative 22; Mismatches 49; Indels 7; Gaps 4;
Qy 3 PVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEV-HNAKTKPR 61
Db 2 PAVTPSVILPPPSSEEL---LKNKATLVCLISDFYPR--TVKVNKADGNSVTQGVDTTP 57
Qy 62 EEQFNSTFRVSVLVTVVHQDWLNGKEYCKVKSNKGLPSSIEKTIK 106
Db 58 SKOSNNKYAASSFLHNTANQWKSQSVTCQVTHEG--HTVEKSLA 100

RESULT 11
KAC6_RABIT
ID -KAC6_RABIT STANDARD; PRT; 104 AA.
AC P03984;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Ig kappa chain b5 variant C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (CLONE PKB5-E2).
RX MEDLINE=84041515; PubMed=6314281;
RA Barnstein K.E., Skurla R.M. Jr., Mage R.G.;
RT "The sequences of rabbit kappa light chains of b4 and b5 allotypes
RT differ more in their constant regions than in their 3' untranslated
RT regions.";
RL Nucleic Acids Res. 11:7205-7214(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=6424123;
RA Smorine L., Sogn J.A., Trinh D., Kindt T.J., Max E.E.;
RT "A genomic gene encoding the b5 rabbit immunoglobulin kappa constant
RT region: implications for latent allotype phenomenon.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1789-1793(1984).
CC -I- MISCELLANEOUS: The cDNA from which this sequence was derived
CC contains a terminator codon within the V-region coding region. The
CC origin of this codon and of the differences between this and other
CC sequenced b5 C regions are unclear. The cDNA clone was made using
CC mRNA from trypanosome-infected b5-homozygous rabbits.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; X00032; -; NOT ANNOTATED_CDS.
DR EMBL; K01363; AAA31355.1; -.
DR PIR; A02124; KSRBV.
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGL1; 1.
DR PROSITE; PS00835; IGLIKE; 1.
DR PROSITE; PS00290; IGMHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON TER 1 1
FT DOMAIN 5 100 Ig-like.
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
FT CONFLICT 1 1 A -> VA (in Ref. 2).
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 17.2%; Score 100; DB 1; Length 104;
Best Local Similarity 25.7%; Pred. No. 0.03;
Matches 27; Conservative 25; Mismatches 41; Indels 12; Gaps 5;
Qy 7 PSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDG----VEVHNAKTKPR 62
Db 5 PTVLIFPPSPAE--LATGATATIVCV---ANKYFPDGTVTWQVDGKPLTTGIETSKTPQNS 59
Qy 63 EEQFNSTFRVSVLVTVVHQDWLNGKEYCKVKSNKGLPSSIEKTIK 107
Db 60 D--DCTYNLSSTLTLSDEYNHDEYTCQVA--QSGSGSPVVSFQR 101

RESULT 12
LAC1_RAT
ID -LAC1_RAT STANDARD; PRT; 104 AA.
AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
RT and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; M22520; AAA41419.1; ALT_INIT.
DR HSP; P01843; IJNH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85
FT DISULFID 103 103 Interchain (with heavy chain).
FT DISULFID 104 AA; 11565 MW; CBF1811F48C878A CRC64;
SQ SEQUENCE 104 AA; 11565 MW; 11565 MW; CBF1811F48C878A CRC64;

Query Match 17.2%; Score 100; DB 1; Length 104;
Best Local Similarity 26.4%; Pred. No. 0.03;
Matches 29; Conservative 23; Mismatches 46; Indels 12; Gaps 5;

OY 3 PVAGPSVFLEPPPKDITLMSRPEVT--CVVDVSHEDPEVO-FWYVDGVEVHAKYK 59
DB 2 PKATPSVTLFPPSSEEL---KTDKATLCVMVDFV---PGVMTVVMKADGTPITQGVET 54
OY 60 PREQFNSTPRVSVLTIVVHODWLNKGYKCKVSNKGLPSSIKTKTISKTK 109
DB 55 TQPFKQNKVMATSYLLLTAKANETHSNYSCQVTHE--ENTVEKSLRAE 102

RESULT 13
KAC MOUSE
ID_KAC_MOUSE STANDARD; PRT; 106 AA.
AC P01837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
RN [2]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).

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RN [3]
RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625; DOI=10.1016/0092-8674(78)90290-8;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an
RT immunoglobulin mRNA using the dideoxynucleotide method of RNA
RT sequencing.";
RL Cell 15:1067-1075(1978).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
RT mouse kappa immunoglobulin J and C region genes.";
RL J. Biol. Chem. 256:5116-5120(1981).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin
RT kappa chain.";
RL Nucleic Acids Res. 9:971-981(1981).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=8329081; PubMed=3138116;
RA de Vaele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
RT directed against the tumour marker human placental alkaline
RT phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; V00807; CAA24189.1; -.
DR PIR; B90262; KIMS.
DR PDB; 1A1F; X-ray; A/L=1-106.
DR PDB; 1FSK; X-ray; B/B=1-106.
DR PDB; 1KB5; X-ray; L=1-106.
DR PDB; 1KCR; X-ray; L=1-106.
DR PDB; 1KCS; X-ray; L=1-106.
DR PDB; 1KCU; X-ray; L=1-106.
DR PDB; 1KCV; X-ray; L=1-106.
DR PDB; 1ORQ; X-ray; A=1-106.
DR PDB; 1ORS; X-ray; A=1-106.
DR PDB; 25C8; X-ray; L=1-103.
DR MGD; MGI:96495; Igk-C.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 5 102 Ig-like.
FT DISULFID 26 86
FT DISULFID 106 106 Interchain (with a heavy chain).

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FT STRAND 3 3
FT STRAND 6 10
FT HELIX 14 17
FT TURN 18 20
FT STRAND 21 32
FT STRAND 37 42
FT STRAND 43 44
FT STRAND 45 47
FT TURN 49 50
FT STRAND 51 55
FT TURN 60 62
FT STRAND 65 74
FT HELIX 75 79
FT TURN 80 80
FT STRAND 83 89
FT TURN 91 92
FT STRAND 97 102
FT TURN 103 106
SQ SEQUENCE 106 AA; 11778 MW; 4B51PF5EF49BAEBS CRC64;

Query Match 17.2%; Score 100; DB 1; Length 106;
Best Local Similarity 24.3%; Pred. No. 0.03;
Matches 26; Conservative 25; Mismatches 50; Indels 6; Gaps 3;

Qy 5 AGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNA--KTKPRE 62
Db 3 AAPTSTVSPSSSEQ--LTSGGASVVCFLNNFPKQ--INVKKIDGSRQNGVLNWTQ 58
Qy 63 EQFNSTRFRVSVLTVDHQLNGKEYKCKVSNKGLPSSIEKTSKTK 109
Db 59 DSKDSTMSMSTLTVDKDEYHRHNSYTCETHKTSSTPIVKSFRNE 105

RESULT 14
KACB RABIT
ID KACB RABIT STANDARD; PRT; 106 AA.
AC P01833;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa-b4 chain C region.
GN Name=K-BAS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Basilea;
RX PubMed=11894960;
RA Heilmann O., Rougeon F.;
RT "Multiplicity of constant kappa light chain genes in the rabbit
RL genome: a b4b4 homozygous rabbit contains a kappa-bas gene.";
CC ENBO J. 2:437-441(1983).
CC -1- MISCELLANEOUS: In Basilea rabbits, the major type of light chain
CC is lambda. The kappa chain shown is a minor component. All other
CC rabbit B allotypes have Cys-64.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; V01241; CAA24558.1; -
CC EMBL; V00885; -; NOT_ANNOTATED_CDS.
DR PIR; A02121; K4RBBS.
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
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DR Pfam; PF00047; ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 87
FT DISULFID 106 106 Interchain (with a heavy chain).
SQ SEQUENCE 106 AA; 11279 MW; AF9B928DDA853849 CRC64;

Query Match 16.6%; Score 96; DB 1; Length 106;
Best Local Similarity 28.4%; Pred. No. 0.076;
Matches 31; Conservative 22; Mismatches 44; Indels 12; Gaps 6;

Qy 3 PVAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVE---VHNAKT 58
Db 3 PVA-PSVLLFPSPKEE--LTGTATIVCVANKFPSPD--ITVTWKVDGTTQQSGIENSKT 57
Qy 59 KPREQFNSTRFRVSVLTVDHQLNGKEYKCKVSNKGLPSSIEKTSK 107
Db 58 POSPE--DNTYLSLSLSTLSLTAQYNHSHSVYTCVV--QGSASPIVQSFNR 103

RESULT 15
KACB RAT
ID KACB RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain C region, B allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Louvain;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong selection
RL at the level of nucleotide sequence.";
RN Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
CC [2]
CC SEQUENCE (BENCE-JONES PROTEIN S211).
CC MEDLINE=75212238; PubMed=807630;
CC Starace V., Querinjean P.;
CC "The primary structure of a rat kappa Bence Jones protein:
CC phylogenetic relationships of V- and C-region genes.";
CC J. Immunol. 115:59-62(1975).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93901; KIRTB.
DR HSSP; P01837; IORS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 5 102 Ig-like.
FT DISULFID 26 86 Interchain (with a heavy chain).
FT DISULFID 106 106 D -> N (in Ref. 2).
FT CONFLICT 2 2 N -> K (in Ref. 2).
FT CONFLICT 30 30 Missing (in Ref. 2).
FT CONFLICT 48 48 E -> Q (in Ref. 2).
FT CONFLICT 79 79 E -> Q (in Ref. 2).
FT CONFLICT 87 87 E -> Q (in Ref. 2).
FT CONFLICT 98 98 V -> VW (in Ref. 2).
FT CONFLICT 100 100 S -> N (in Ref. 2).
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.3927 Seconds  
(without alignments)  
347.833 Million cell updates/sec

Title: US-09-674-857-2  
Perfect score: 590  
Sequence: 1 APPVAGSVFLFPKPKDTL.....CKVSNKGLPSIEKTIKTK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0  
Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	98.6	109	3	US-08-444-644-30
2	572	98.6	109	3	US-08-232-246A-30
3	536	92.4	109	2	US-08-070-116A-4
4	536	92.4	109	4	US-08-557-050-4
5	536	92.4	110	3	US-08-444-644-44
6	536	92.4	110	3	US-08-232-246A-44
7	523	90.2	110	3	US-08-444-644-21
8	523	90.2	110	3	US-08-232-246A-21
9	522	90.0	105	2	US-08-232-539D-60
10	514	88.6	110	3	US-08-444-644-38
11	514	88.6	110	3	US-08-232-246A-38
12	321	55.3	66	3	US-08-569-147-85
13	175	30.2	107	4	US-09-281-760E-36
14	172.5	29.7	106	2	US-08-232-539D-54
15	158	27.2	109	3	US-08-466-163B-1
16	158	27.2	109	4	US-09-802-096-1
17	158	27.2	109	4	US-09-802-077-1
18	138	23.8	100	1	US-08-422-101-10
19	138	23.8	100	1	US-08-422-091-10
20	138	23.8	100	2	US-08-422-092-10
21	138	23.8	100	2	US-08-788-800-7
22	138	23.8	100	3	US-08-422-093-10
23	135	23.8	100	3	US-08-422-112-10
24	135	23.3	105	3	US-09-025-769B-166
25	135	23.3	105	4	US-09-490-070A-166
26	135	23.3	105	4	US-09-490-153-166
27	135	23.3	105	4	US-09-490-324-166

28 135 23.3 106 2 US-08-378-939-40 Sequence 40, Appl  
29 135 23.3 106 2 US-08-761-277A-49 Sequence 49, Appl  
30 135 23.3 106 3 US-08-444-644-26 Sequence 26, Appl  
31 135 23.3 106 3 US-08-232-246A-26 Sequence 26, Appl  
32 135 23.3 107 1 US-08-422-101-8 Sequence 8, Appl  
33 135 23.3 107 1 US-08-422-091-8 Sequence 8, Appl  
34 135 23.3 107 2 US-08-422-092-8 Sequence 8, Appl  
35 135 23.3 107 2 US-08-788-800-5 Sequence 5, Appl  
36 135 23.3 107 3 US-08-422-093-8 Sequence 8, Appl  
37 135 23.3 107 3 US-08-422-112-8 Sequence 8, Appl  
38 135 23.3 107 4 US-09-301-593-20 Sequence 20, Appl  
39 135 23.3 108 4 US-09-313-942-13 Sequence 13, Appl  
40 131 22.6 106 1 US-08-399-106A-7 Sequence 7, Appl  
41 131 22.6 106 1 US-08-433-105A-7 Sequence 7, Appl  
42 131 22.6 106 2 US-08-434-869A-7 Sequence 7, Appl  
43 126 21.7 106 2 US-08-378-939-42 Sequence 42, Appl  
44 124.5 21.5 109 2 US-08-646-981-6 Sequence 6, Appl  
45 124 21.4 109 1 US-08-436-463-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-08-444-644-30  
; Sequence 30, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-30

Query Match      98.6%; Score 572; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 1.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
DB 1 APPVAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
DB 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTIISKTK 109

RESULT 3
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 585573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-070-116A-4

Query Match      92.4%; Score 536; DB 2; Length 109;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPRE 63
DB 4 LGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPRE 63
QY 64 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKTK 109
DB 64 QFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIISKAK 109

RESULT 4
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
```

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; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-050-4

Query Match 92.4%; Score 536; DB 4; Length 109;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKPREE 63
Db 4 LGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKPREE 63

Qy 64 QFNSTRVWSVLTIVHQDLNGLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 64 QFNSTRVWSVLTIVHQDLNGLNGKEYCKVSNKGLPSSIEKTIKTK 109

RESULT 5
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-050-4

Query Match 92.4%; Score 536; DB 4; Length 109;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKPREE 63
Db 4 LGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKPREE 63

Qy 64 QFNSTRVWSVLTIVHQDLNGLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 64 QFNSTRVWSVLTIVHQDLNGLNGKEYCKVSNKGLPSSIEKTIKTK 109

RESULT 5
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-44

Query Match 92.4%; Score 536; DB 3; Length 110;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKPREE 63
Db 5 LGGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVHNAKTKPREE 64

Qy 64 QFNSTRVWSVLTIVHQDLNGLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QFNSTRVWSVLTIVHQDLNGLNGKEYCKVSNKGLPSSIEKTIKTK 110

RESULT 6
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-44

Query Match 92.4%; Score 536; DB 3; Length 110;
Best Local Similarity 94.3%; Pred. No. 2.8e-55;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 64 QFNSTRVSVLTVHVDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 65 QFNSTRVSVLTVHVDWLNGKEYCKVSNKGLPSSIEKTIKSKAK 110
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-21

Query Match 90.2%; Score 523; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 9.5e-54;
Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 64 QFNSTRVSVLTVHVDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 65 QYNSTRVSVLTVHVDWLNGKEYCKVSNKGLPAPIEKTISKAK 110
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240

```

```
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21

Query Match          90.2%; Score 523; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 9.5e-54;
Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTPREE 63
Db 5 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTPREE 64

QY 64 QFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QYNSTFRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTIKAK 110

RESULT 9
US-08-232-539D-60
; Sequence 60, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: 1ge Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-60

Query Match          90.0%; Score 522; DB 2; Length 105;
Best Local Similarity 92.3%; Pred. No. 1.2e-53;
Matches 96; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTPREEQF 65

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21

Query Match          90.2%; Score 523; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 9.5e-54;
Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTPREE 63
Db 5 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTPREE 64

QY 64 QFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QYNSTFRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTIKAK 110

RESULT 10
US-08-444-644-38
; Sequence 38, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-38

Query Match          88.6%; Score 514; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 1.1e-52;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTPREE 63
Db 5 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTLREE 64

QY 64 QFNSTFRVSVLTVVHQDMLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QYNSTFRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTIKAK 110
```

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RESULT 11
US-08-232-246A-38
; Sequence 38, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA: US 07/404,089
; APPLICATION NUMBER: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-38

Query Match      88.6%; Score 514; DB 3; Length 110;
Best Local Similarity 90.6%; Pred. No. 1.1e-52;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
Db      5 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKLREE 64

QY      64 QFNSTFRVSVLTIVVHQDWLNGKEYKCKVSNKGLPSSIEKTK 109
Db      65 QYNSTFRVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
```

```
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-85

Query Match      55.3%; Score 321; DB 3; Length 66;
Best Local Similarity 93.5%; Pred. No. 2.5e-30;
Matches 58; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
Db      5 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 64

QY      64 QF 65
Db      65 QY 66

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)-(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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Db 65 NGTLVTSTLPVGTDRWIEG-ETQCRVTHPHLPALMRSTTKT 106

Search completed: November 17, 2005, 07:53:55  
Job time : 23.3927 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:47:15 ; Search time 82.3721 Seconds  
(without alignments)  
553.666 Million cell updates/sec

Title: US-09-674-857-2  
Perfect score: 580  
Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 892101

Minimum DB seq length: 0  
Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*  
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19: /cgn2\_6/ptodata/1/pubaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES										
Result No.	Score	Query Match	Length	ID	Description	Sequence	2, Appli	Sequence	17, Appl	Sequence
1	572	98.6	109	18	US-10-959-318-2	Sequence 2, Appli	Sequence 2, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl
2	564	97.2	109	18	US-10-959-318-17	Sequence 17, Appl	Sequence 17, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl
3	564	97.2	109	18	US-10-959-318-18	Sequence 18, Appl	Sequence 18, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl
4	554	95.5	109	18	US-10-959-318-11	Sequence 11, Appl	Sequence 11, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 12, Appl
5	554	95.5	109	18	US-10-959-318-12	Sequence 12, Appl	Sequence 12, Appl	Sequence 9, Appl	Sequence 9, Appl	Sequence 9, Appl
6	543.5	93.7	110	18	US-10-959-318-9	Sequence 9, Appl	Sequence 9, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl
7	543.5	93.7	110	18	US-10-959-318-10	Sequence 10, Appl	Sequence 10, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl
8	540	93.1	109	18	US-10-959-318-15	Sequence 15, Appl	Sequence 15, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl
9	540	93.1	109	18	US-10-959-318-16	Sequence 16, Appl	Sequence 16, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 25, Appl
10	538.5	92.8	110	20	US-11-018-102-25	Sequence 25, Appl	Sequence 25, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli
11	536	92.4	109	14	US-10-267-286A-4	Sequence 4, Appli	Sequence 4, Appli			

12	536	92.4	110	18	US-10-959-318-4	Sequence 4, Appli	Sequence 4, Appli			
13	536	92.4	110	18	US-10-959-318-21	Sequence 21, Appl	Sequence 21, Appl			
14	536	92.4	110	20	US-11-018-102-24	Sequence 24, Appl	Sequence 24, Appl			
15	529.5	91.3	110	18	US-10-959-318-13	Sequence 13, Appl	Sequence 13, Appl			
16	529.5	91.3	110	18	US-10-959-318-14	Sequence 14, Appl	Sequence 14, Appl			
17	529	91.2	110	18	US-10-959-318-3	Sequence 3, Appli	Sequence 3, Appli			
18	529	91.2	110	18	US-10-959-318-7	Sequence 7, Appli	Sequence 7, Appli			
19	529	91.2	110	18	US-10-959-318-8	Sequence 8, Appli	Sequence 8, Appli			
20	528	91.0	109	18	US-10-627-556-270	Sequence 270, App	Sequence 270, App			
21	525.5	90.6	110	20	US-11-018-102-23	Sequence 23, Appl	Sequence 23, Appl			
22	523	90.2	109	14	US-10-207-655-220	Sequence 220, App	Sequence 220, App			
23	523	90.2	109	18	US-10-627-556-14	Sequence 14, Appl	Sequence 14, Appl			
24	523	90.2	110	15	US-10-370-749-23	Sequence 23, Appl	Sequence 23, Appl			
25	523	90.2	110	18	US-10-959-318-1	Sequence 1, Appli	Sequence 1, Appli			
26	523	90.2	110	20	US-11-018-102-22	Sequence 22, Appl	Sequence 22, Appl			
27	522	90.0	102	18	US-10-609-783B-57	Sequence 57, Appl	Sequence 57, Appl			
28	522	90.0	102	18	US-10-609-783B-59	Sequence 59, Appl	Sequence 59, Appl			
29	522	90.0	109	18	US-10-627-556-302	Sequence 302, App	Sequence 302, App			
30	521	89.8	110	18	US-10-959-318-19	Sequence 19, Appl	Sequence 19, Appl			
31	521	89.8	110	18	US-10-959-318-20	Sequence 20, Appl	Sequence 20, Appl			
32	519	89.5	109	18	US-10-627-556-294	Sequence 294, App	Sequence 294, App			
33	518	89.3	109	14	US-10-020-354-80	Sequence 80, Appl	Sequence 80, Appl			
34	518	89.3	109	18	US-10-627-556-258	Sequence 258, App	Sequence 258, App			
35	518	89.3	109	18	US-10-627-556-278	Sequence 278, App	Sequence 278, App			
36	518	89.3	110	15	US-10-370-749-53	Sequence 53, Appl	Sequence 53, Appl			
37	516	89.0	110	15	US-10-370-749-51	Sequence 51, Appl	Sequence 51, Appl			
38	516	89.0	110	18	US-10-959-318-22	Sequence 22, Appl	Sequence 22, Appl			
39	515	88.8	109	14	US-10-207-655-322	Sequence 322, App	Sequence 322, App			
40	515	88.8	109	18	US-10-627-556-92	Sequence 92, Appl	Sequence 92, Appl			
41	515	88.8	110	18	US-10-959-318-5	Sequence 5, Appli	Sequence 5, Appli			
42	515	88.8	110	18	US-10-959-318-6	Sequence 6, Appli	Sequence 6, Appli			
43	515	88.8	110	18	US-10-959-318-25	Sequence 25, Appl	Sequence 25, Appl			
44	514	88.6	110	18	US-10-959-318-23	Sequence 23, Appl	Sequence 23, Appl			
45	514	88.6	110	18	US-10-959-318-24	Sequence 24, Appl	Sequence 24, Appl			

ALIGNMENTS

RESULT 1  
US-10-959-318-2  
; Sequence 2, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; APPLICANT: Clark, Michael R  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 2  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-959-318-2

Query Match		98.6%	Score 572;	DB 18;	Length 109;
Best Local Similarity		98.2%	Pred. No. 1.6e+48;		
Matches 107;		Conservative	1;	Mismatches	0; Gaps 0;
Qy	1	APPVAGPSVFLFPKPKDTLMI	SRTPEVTCVVVDVSHEDDEVGFVN	WVVDGVVHNATKP	60
Db	1	APPVAGPSVFLFPKPKDTLMI	SRTPEVTCVVVDVSHEDDEVGFVN	WVVDGVVHNATKP	60
Qy	61	REEQFNSTFRVSVLT	VVHODWLNKGEYKCKVSNKGLP	SSIEKTIKTK	109
Db	61	REEQFNSTFRVSVLT	VVHODWLNKGEYKCKVSNKGLP	SSIEKTIKTK	109

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RESULT 2
US-10-959-318-17
; Sequence 17, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta d (D268) mutation
US-10-959-318-17

Query Match          97.2%; Score 564; DB 18; Length 109;
Best Local Similarity 97.2%; Pred. No. 9.6e-48;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIKTK 109

RESULT 3
US-10-959-318-18
; Sequence 18, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta e (E268) mutation
US-10-959-318-18

Query Match          97.2%; Score 564; DB 18; Length 109;
Best Local Similarity 97.2%; Pred. No. 9.6e-48;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSEDPVFQFNWYVDGVEVHNAKTKP 60
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QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIKTK 109

RESULT 4
US-10-959-318-11
; Sequence 11, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
US-10-959-318-11

Query Match          95.5%; Score 554; DB 18; Length 109;
Best Local Similarity 94.5%; Pred. No. 9.2e-47;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 61 REEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109

RESULT 5
US-10-959-318-12
; Sequence 12, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and e (E268)
US-10-959-318-12

Query Match          95.5%; Score 554; DB 18; Length 109;
Best Local Similarity 94.5%; Pred. No. 9.2e-47;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 60
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Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Qy 61 REEQFNSTFRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIKTK 109
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Db 61 REEQNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKSKAK 109
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RESULT 6
US-10-959-318-9
; Sequence 9, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)
US-10-959-318-9

Query Match 93.7%; Score 543.5; DB 18; Length 110;
Best Local Similarity 93.6%; Pred. No. 1e-45;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 59
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Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Qy 60 PREQFNSTFRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIKTK 109
|||||
Db 61 PREEQNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKSKAK 110
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RESULT 7
US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and e (E268)
US-10-959-318-10

Query Match 93.7%; Score 543.5; DB 18; Length 110;
Best Local Similarity 93.6%; Pred. No. 1e-45;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 59
|||||
Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Qy 60 PREQFNSTFRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIKTK 109
|||||
Db 61 PREEQNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKSKAK 110
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RESULT 8
US-10-959-318-11
; Sequence 11, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and d (D269)
US-10-959-318-11

Query Match 93.1%; Score 540; DB 18; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.2e-45;
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 60
|||||
Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Qy 61 REEQFNSTFRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIKTK 109
|||||
Db 61 REEQNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKSKAK 109
|||||

RESULT 9
US-10-959-318-16
; Sequence 16, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 109
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US-10-959-318-10
Query Match 93.7%; Score 543.5; DB 18; Length 110;
Best Local Similarity 93.6%; Pred. No. 1e-45;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 59
|||||
Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Qy 60 PREQFNSTFRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIKTK 109
|||||
Db 61 PREEQNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKSKAK 110
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RESULT 8
US-10-959-318-15
; Sequence 15, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and d (D269)
US-10-959-318-15

Query Match 93.1%; Score 540; DB 18; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.2e-45;
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 60
|||||
Db 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Qy 61 REEQFNSTFRVSVLTVVHQDNLGKEYCKVSNKGLPSSIEKTIKTK 109
|||||
Db 61 REEQNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKSKAK 109
|||||

RESULT 9
US-10-959-318-16
; Sequence 16, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 109
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```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-16

Query Match      93.1%; Score 540; DB 18; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.2e-45;
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 1 APPVAGSVFLFPKPKDGLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP 60

Qy 61 REQNFSTPRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 REQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTIKSKAK 109

RESULT 10
US-11-018-102-25
; Sequence 25, Application US/11018102
; Publication No. US20050136061A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5045 USA NP
; CURRENT APPLICATION NUMBER: US/11/018,102
; CURRENT FILING DATE: 2004-12-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: engineered G4 CH2
US-11-018-102-25

Query Match      92.8%; Score 538.5; DB 20; Length 110;
Best Local Similarity 93.6%; Pred. No. 3.1e-45;
Matches 103; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 APPVA-GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
Db 1 APEAAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTK 60

Qy 60 PREEQNFSTPRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 61 PREEQNFSTYRVSVLTVLHQDNLNGKEYCKVSNKGLPSSIEKTIKSKAK 110

RESULT 11
US-10-267-286A-4
; Sequence 4, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/10/267,286A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-4

Query Match      92.4%; Score 536; DB 14; Length 109;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
Db 4 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREE 63

Qy 64 QFNSTPRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 64 QFNSTYRVSVLTVLHQDNLNGKEYCKVSNKGLPSSIEKTIKSKAK 109

RESULT 12
US-10-959-318-4
; Sequence 4, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-318-4

Query Match      92.4%; Score 536; DB 18; Length 110;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREE 64

Qy 64 QFNSTPRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 65 QFNSTYRVSVLTVLHQDNLNGKEYCKVSNKGLPSSIEKTIKSKAK 110

RESULT 13
US-10-959-318-21
; Sequence 21, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
```

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; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG4 CH2 sequence with delta e (E368) mutation
US-10-959-318-21

Query Match          92.4%; Score 536; DB 18; Length 110;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSEDEPEVFQFNWYVDGVEVHNAKTKPREE 64
Qy 64 QFNSTFRVSVSLTVVHODWLNKGKEYCKVSNKGLPSSIETISKT 109
Db 65 QFNSTYRVSVSLTVLHQDWLNGKEYCKVSNKGLPSSIETISKAK 110

RESULT 14
US-11-018-102-24
; Sequence 24, Application US/11018102
; Publication No. US20050136061A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5045 USA NP
; CURRENT APPLICATION NUMBER: US/11/018.102
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-018-102-24

Query Match          92.4%; Score 536; DB 20; Length 110;
Best Local Similarity 94.3%; Pred. No. 5.5e-45;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VAGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 5 LGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSEDEPEVFQFNWYVDGVEVHNAKTKPREE 64
Qy 64 QFNSTFRVSVSLTVVHODWLNKGKEYCKVSNKGLPSSIETISKT 109
Db 65 QFNSTYRVSVSLTVLHQDWLNGKEYCKVSNKGLPSSIETISKAK 110

RESULT 15
US-10-959-318-13
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959.318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
US-10-959-318-13

Query Match          91.3%; Score 529.5; DB 18; Length 110;
Best Local Similarity 90.9%; Pred. No. 2.4e-44;
Matches 100; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 1 APPVA-GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 59
Db 1 APPVAGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSEDEPEVFQFNWYVDGVEVHNAKTK 60
Qy 60 PREEQFNSTFRVSVSLTVVHODWLNKGKEYCKVSNKGLPSSIETISKT 109
Db 61 PREEQFNSTYRVSVSLTVLHQDWLNGKEYCKVSNKGLPSSIETISKAK 110

Search completed: November 17, 2005, 08:18:46
Job time : 83.3721 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 91.6667 Seconds  
(without-alignments)  
464.112 Million cell updates/sec

Title: US-09-674-857-3  
Perfect score: 587  
Sequence: 1 APPVAGGSFVFLPPKPKDT.....CKVSNKGLPSSIEKTIISKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	98.1	110	3 AAY54998	Mutated C
2	570.5	97.2	109	3 AAY54996	Mutated C
3	570	97.1	435	7 ADM33857	Human HuE
4	570	97.1	435	8 ADM33857	Human HuE
5	570	97.1	447	7 ADM33380	Human GCS
6	562	95.7	468	2 AAW85689	Human GCS
7	562	95.7	488	3 AAY97175	Human FGF
8	562	95.7	497	3 AAY97174	Human FGF
9	562	95.7	525	3 AAY97173	Human FGF
10	562	95.7	711	2 AAW85692	MotABII f
11	561	95.6	447	6 AAE33524	Human AQC
12	560	95.4	251	6 AAE35231	Human imm
13	558	95.1	232	5 ABB81492	Human mut
14	558	95.1	232	5 ABB81491	Human mut
15	558	95.1	250	6 AAE35220	Human mod
16	558	95.1	251	2 AAY05688	Modified
17	558	95.1	251	2 AAW97756	Modified
18	558	95.1	251	3 AAB07541	Amino aci
19	558	95.1	251	6 AAE35218	Human mod
20	558	95.1	251	6 AAE35219	Human imm
21	558	95.1	328	5 ABB81493	Ztnfr12-t
22	558	95.1	332	6 AAE35228	Human TAC
23	558	95.1	344	6 AAE35224	Human TAC
24	558	95.1	348	6 AAE35225	Human TAC
25	558	95.1	357	6 AAE35226	Human TAC

26	558	95.1	392	6 AAE35223	Human TAC
27	558	95.1	437	7 ADM33855	Human HuE
28	558	95.1	437	8 ADM33855	Human HuE
29	558	95.1	449	7 ADM33378	Human GCS
30	558	95.1	473	5 ABB81645	Zcytor19
31	558	95.1	473	7 ADF83613	Cytokine
32	558	95.1	476	5 AAU76912	Human CRF
33	558	95.1	476	6 AAE30845	Human CRF
34	558	95.1	484	5 AAU76916	Human zcy
35	558	95.1	484	6 AAE30844	Human zcy
36	558	95.1	484	7 ABR83693	hzcycor11
37	558	95.1	556	5 AAE29073	Human IL-
38	558	95.1	559	4 AAB85286	IL-20RA-I
39	558	95.1	559	5 AEG67217	IL-20RA e
40	558	95.1	559	5 AEG67217	Human IL-
41	558	95.1	559	8 ADJ83342	Human IL-
42	558	95.1	573	5 AAE29072	Human IL-
43	558	95.1	594	4 AAB85274	Human IL-
44	558	95.1	594	4 AAU04062	Human IL-
45	558	95.1	594	5 AEG67205	IL-20RA e

## ALIGNMENTS

### RESULT 1

AAY54998  
ID AAY54998 standard; protein; 110 AA.

XX AC AAY54998;

XX AC AAY54998;

DT 17-FEB-2000 (first entry)

XX DE Mutated CH2 sequence Gideltaac.

XX DE Mutated CH2 sequence Gideltaac.

KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;  
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
KW sickle cell anaemia; coronary artery occlusion.

XX OS Synthetic.

XX OS Synthetic.

PN WO9958572-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001441.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

XX PR 08-MAY-1998; 98GB-00009951.

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
CC molecule is used to bind a target molecule (especially FcγmαRIIb  
CC causing inhibition of B cell activation, mast cell degranulation or  
CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
CC binding of a second binding molecule, e.g. an antibody, to the target  
CC molecule. The binding molecule is useful for the treatment of graft-vs-  
CC host disease, organ transplant rejection, bone-marrow transplant  
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.  
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
CC coronary artery occlusion). The binding molecules do not activate  
CC complement or trigger cytotoxic activities through FcγmαRIIb  
CC IgG properties have been retained. The polypeptides do not contain non-  
CC human amino acids, and are therefore likely to have reduced  
CC immunogenicity. Further, they still bind Protein A, which is consistent  
CC with being able to cross the human placenta through interaction with FcRn  
CC (neonatal Fc receptor)  
XX  
SQ Sequence 110 AA;

Query Match 98.1%; Score 576; DB 3; Length 110;  
Best Local Similarity 99.1%; Pred. No. 1.4e-51;  
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
QY 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110  
DB 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

RESULT 2  
ID AAY54996 standard; protein; 109 AA.  
XX AAY54996;  
XX  
DT 17-FEB-2000 (first entry)  
DE Mutated CH2 sequence G1deltaaab.  
XX  
KW Binding molecule; CH2 sequence; complement dependent lysis; FcγmαRIIb;  
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
KW bone-marrow transplant rejection; autoimmunity disease; asthma; allergy;  
KW alloimmune disorder; autoimmunity haemolytic anaemia; inflammatory disease;  
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
KW sickle cell anaemia; coronary artery occlusion.  
XX  
OS Synthetic.  
XX  
PN WO9958572-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001441.  
XX  
PR 08-MAY-1998; 98GB-00009951.  
XX  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX  
PI Armour KL, Clark MR, Williamson LM;  
XX  
DR WPI; 2000-039075/03.  
XX  
XX Immunoglobulin-derived binding molecules that do not activate complement  
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin

PT properties.  
XX  
PS Claim 12; Fig 17; 81pp; English.  
XX  
CC This sequence represents the mutated CH2 molecule G1deltaab, and is a  
CC binding molecule of the invention. The recombinant binding molecule is  
CC capable of binding a target molecule without triggering complement  
CC dependent lysis, or the cell-mediated destruction of the target  
CC host disease, organ transplant rejection, bone-marrow transplant  
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.  
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
CC coronary artery occlusion). The binding molecules do not activate  
CC complement or trigger cytotoxic activities through FcγmαRIIb and desirable  
CC IgG properties have been retained. The polypeptides do not contain non-  
CC human amino acids, and are therefore likely to have reduced  
CC immunogenicity. Further, they still bind Protein A, which is consistent  
CC with being able to cross the human placenta through interaction with FcRn  
CC (neonatal Fc receptor)  
XX  
SQ Sequence 109 AA;

Query Match 97.2%; Score 570.5; DB 3; Length 109;  
Best Local Similarity 99.1%; Pred. No. 5.3e-51;  
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59  
QY 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110  
DB 60 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 109

RESULT 3  
ADM33857  
ID ADM33857 standard; protein; 435 AA.  
XX ADM33857;  
AC ADM33857;  
DT 03-JUN-2004 (first entry)  
DE Human HuEPO-L-vFcγmαRII fusion protein.  
XX  
KW Erythropoietin; EPO; immunoglobulin; IgG;  
KW fragment crystallisation region; Fc; chronic anaemia; renal disease;  
KW cancer chemotherapy; rheumatoid arthritis; AIDS;  
KW myelodysplastic syndrome; (HuEPO)-L-vFcγmαRII; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..27  
FT /note= "Signal peptide"  
FT Protein 28..192  
FT /note= "EPO"  
FT Peptide 193..208  
FT /note= "Linker"  
FT Protein 209..435  
FT /note= "IgG1 Fc"  
FT Misc-difference 222



FT Misc-difference 318 /note= "Wild-type Leu substituted by Val"  
FT /note= "Wild-type Leu substituted by Ala"

US2003082749-A1.  
01-MAY-2003.  
17-AUG-2001; 2001US-00932812.  
17-AUG-2001; 2001US-00932812.  
(SUNL/) SUN L K.  
(SUNB/) SUN B N C.  
(SUNC/) SUN C R Y.

Sun LK, Sun BNC, Sun CRY;  
WPI; 2003-616080/58.  
N-PSDB; ADM33856.

New recombinant human erythropoietin-L-vFc fusion proteins, useful for treating patients with chronic anemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV infection.

Claim 5; Fig 2C; 14pp; English.

The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc fusion protein comprising HuEPO, a peptide linker, and a human immunoglobulin G Fc (fragment crystallisation region) variant. Also included is a carbohydrate-derived cell line producing the human erythropoietin-L-vFc fusion protein cited above in its growth medium in excess of 10 microgramme per million cells in a 24-hour period. The HuEPO-L-vFc fusion protein exhibits an enhanced in vitro biological activity of at least 2-fold relative to that of recombinant HuEPO on a molar basis. The flexible peptide linker containing about 20 or fewer amino acids is present between HuEPO and the human IgG Fc variant. The IgG Fc contains amino acid mutations to attenuate effector functions. The human IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with Pro331Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The recombinant human erythropoietin-L-vFc fusion proteins are useful for treating patients with chronic anaemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV infection, or myelodysplastic syndrome. The increased activity and prolonged presence of the human erythropoietin-L-vFc fusion protein in the serum, as compared to prior art, leads to lower dosages and less frequent injections. Less fluctuations of the drug in serum concentrations means improved safety and tolerability, and less frequent injections result in better patient compliance and quality of life. The present sequence represents the fusion protein HuEPO-L-vFc gamma1.

XX Sequence 435 AA;

Query Match 97.1%; Score 570; DB 7; Length 435;  
Best Local Similarity 97.3%; Pred. No. 3.2e-50;  
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 219 APEVAGGSPVFLPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278  
QY 61 PREEQYNSTRYRVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIKSAK 110  
Db 279 PREEQYNSTRYRVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIKSAK 328

RESULT 4  
ADR48988  
ID ADR48988 standard; protein; 435 AA.  
XX  
AC ADR48988;

XX 02-DEC-2004 (first entry)  
XX HuEPO-L-vFc fusion protein #2.  
XX antianemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;  
KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;  
KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.  
XX Homo sapiens.  
OS Synthetic.  
XX US2004175824-A1.  
XX 09-SEP-2004.  
XX 21-JAN-2004; 2004US-00761593.  
XX 17-AUG-2001; 2001US-00932812.  
XX (SUNL/) SUN L K.  
XX (SUNB/) SUN B N C.  
XX (SUNC/) SUN C R Y.  
XX Sun LK, Sun BNC, Sun CRY;  
XX WPI; 2004-634851/61.  
XX N-PSDB; ADR48987.  
XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.  
XX Claim 5; SEQ ID NO 22; 31pp; English.  
XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, is new.  
XX INDEPENDENT CLAIMS are also included for the following: a chinese hamster ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in its growth medium in excess of 10 microg per million cells in a 24 hour period; and a method for making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred Protein: The peptide linker containing 20 or fewer amino acids is present between HuEPO and the human IgG Fc variant, and comprises two or more amino acids selected from glycine, serine, alanine, and threonine. The human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18). It also comprises a hinge, CH2, and CH3 domains of human IgG4 with Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO. 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1 with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line producing the HuEPO-L-vFc fusion protein in its growth medium in excess of 30 microg per million cells in a 24 hour period. The human IgG Fc variant comprises a hinge, CH2, CH3 domains of human IgG selected from IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, the IgG Fc contains amino acid mutations to attenuate effector functions, a flexible peptide linker containing 20 or fewer amino acids is present between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Preferred Method: Making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human IgG Fc variant comprises: generating a CHO-derived cell line; growing the cell line where the recombinant protein is expressed in its growth medium in excess of 10 microg per million cells in a 24 hour period; and purifying the expressed protein from (b), where the recombinant fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological data given. None given. Administration can be through subcutaneous or intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion

CC protein is useful for treating patients with chronic anemia due to renal  
 CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for  
 CC HIV infection, or myelodysplastic syndrome. It is also useful in the  
 CC treatment of renal failure. A fusion protein was assembled from several  
 CC DNA segments. To obtain the gene encoding the leader peptide and mature  
 CC protein of human erythropoietin (EPO), cDNA library of human fetal liver  
 CC or kidney was used as the template in polymerase chain reaction (PCR).  
 CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a  
 CC restriction enzyme cleavage site is used as the 5' oligonucleotide  
 CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon  
 CC and incorporates a BamHI site. The resulting DNA fragments of  
 CC approximately 600 bp were inserted into a holding vector such as pUC19 at  
 CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the  
 CC human EPO gene was confirmed by DNA sequencing.

XX SQ Sequence 435 AA;

Query Match 97.1%; Score 570; DB 8; Length 435;  
 Best Local Similarity 97.3%; Pred. No. 3.2e-50;  
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
 DB 219 APEVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

DB 279 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTIKAK 328

RESULT 5

ADM33380  
 ID ADM33380 standard; protein; 447 AA.

XX ADM33380;

DT 03-JUN-2004 (first entry)

XX Human GCSF-L-fragment of crystallisation gamma 1 fusion protein.

XX cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy;  
 KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-VFC;  
 KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;  
 KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;  
 KW bone marrow transplantation; chronic neutropenia; fusion protein;  
 KW fragment of crystallisation gamma 1; FC gamma 1.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 234 /note= "Wild type Leu substituted by Val"

FT Misc-difference 235 /note= "Wild type Leu substituted by Ala"

FT Misc-difference 331 /note= "Wild type Pro substituted by Ser"

FT /note= "Wild type Pro substituted by Ser"

XX US2003082679-A1.

XX 01-MAY-2003.

XX 01-OCT-2001; 2001US-00968362.

XX 01-OCT-2001; 2001US-00968362.

XX (SUNL/) SUN L K.

XX (SUNB/) SUN B N C.

XX (SUNC/) SUN C R Y.

XX Sun LK, Sun BNC, Sun CRY;

XX WPI; 2003-585400/55.

DR N-PSDB; ADM33379.

XX New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-  
 PT vFc fusion protein for treating immune or hematopoietic system disorders  
 PT comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G  
 PT FC variant.

XX Disclosure; Fig 2C; 15pp; English.

XX The invention describes a recombinant human granulocyte colony-  
 CC stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a  
 CC peptide linker, and a human immunoglobulin G (IgG) FC variant. Also  
 CC described are: a CHO-derived cell line producing the above hG-CSF-L-vFc  
 CC fusion protein in its growth medium in excess of 10 mg/g per million  
 CC cells in a 24-hour period; and making the recombinant fusion protein  
 CC cited above, comprising generating a CHO-derived cell line cited above,  
 CC growing the cell line under conditions the recombinant fusion protein is  
 CC expressed in its growth medium, and purifying the expressed protein. The  
 CC recombinant fusion protein is useful in treating a variety of conditions  
 CC associated with an impaired immune or hematopoietic system, including  
 CC cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow  
 CC transplantation, and chronic neutropenias. This is the amino acid  
 CC sequence of human GCSF-L-fragment of crystallisation gamma 1 variant  
 CC fusion protein.

XX SQ Sequence 447 AA;

Query Match 97.1%; Score 570; DB 7; Length 447;  
 Best Local Similarity 97.3%; Pred. No. 3.3e-50;  
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

DB 231 APEVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

DB 291 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTIKAK 340

RESULT 6

AAW85689

ID AAW85689 standard; protein; 468 AA.

XX AAW85689;

DT 12-AUG-1999 (first entry)

XX D9D10 heavy chain fusion protein.

XX Antibody; humanised; variable region; heavy chain; light chain;  
 KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;  
 KW immune disease; multiple sclerosis; Crohn's disease; skin disorders;  
 KW inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;  
 KW multivalent; ruminant.

OS Synthetic.

OS Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..20 /note= "D9D10 light chain signal peptide"

FT Domain 21..137 /note= "Humanised heavy chain variable domain of D9D10"

FT Domain 138..467 /note= "Human IgG1 heavy chain constant domain"

FT Misc-difference 468 /note= "Leu added by cloning strategy"

XX WO9909055-A2.

XX 25-FEB-1999.

XX



```

XX SQ Sequence 488 AA;
Query Match 95.7%; Score 562; DB 3; Length 488;
Best Local Similarity 95.5%; Pred. No. 2.5e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 272 APELEGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331
Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 332 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 381

RESULT 8
AA97174
ID AA97174 standard; protein; 497 AA.
XX AC AA97174;
XX DT 04-DEC-2000 (first entry)
XX DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 5.
XX KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnery;
KW ophthalmological; anti-proliferative.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FH Peptide 1..21
FT /label= FGF-R1_signal_peptide
FT Domain 22..257
FT /label= FGF-R1_extracellular_domain
FT /note= "The Ig I segment and acid box are deleted"
FT Domain 59..111
FT /label= Ig_II_segment
FT Domain 157..222
FT /label= Ig_III_segment
FT Peptide 258..265
FT /label= Linker
FT Region 266..497
FT /label= Human IgG1 Fc region
FT /note= "Contains hinge region and domains CH2 and CH3"
FT Misc-difference 285
FT /label= L285E
FT /note= "This mutation decreases the affinity of the Fc
FT portion for Fc receptors"
FT Misc-difference 385
FT /label= P385S
FT /note= "This mutation decreases the affinity of the Fc
FT portion for complement"
XX PN WO200046380-A2.
XX PD 10-AUG-2000.
XX PF 07-FEB-2000; 2000WO-US003166.
XX PR 08-FEB-1999; 99US-0119002P.
XX PA (CHIR ) CHIRON CORP.
XX PI Kavanaugh WM, Ballinger M;
XX WP1; 2000-514961/46.
XX DR N-PSDB; AAA52131.
XX PT New polypeptide comprising a fibroblast growth factor receptor

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PT extracellular domain fused to a heterologous oligomerization domain for
PT treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX Claim 14; Page 65-66; 70pp; English.
XX Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
XX receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
XX (Ig) I segment fused to a heterologous oligomerization domain that
XX comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
XX region, or light chain of an immunoglobulin molecule, or a peptide with a
XX leucine zipper motif. The Ig I segment is not necessary for binding of
XX acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
XX affinity for aFGF and heparin, protects the core of the molecule from
XX proteolysis, and abrogates the heparin requirement for aFGF binding. The
XX new fusion polypeptides are better FGF inhibitors than FGF-R monomer
XX proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at
XX subnanomolar concentrations and were 20-fold more potent than the FGF-R
XX monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
XX fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
XX mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung,
XX rectal, testis and cervical tumours), neovascularization (e.g. diabetic
XX retinopathy, neovascular glaucoma, wound healing and corneal scarring)
XX and hyper-proliferation of vascular smooth muscle cells (e.g.
XX postangioplasty and postatherectomy restenosis)
XX SQ Sequence 497 AA;
Query Match 95.7%; Score 562; DB 3; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.5e-49;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 281 APELEGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340
Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 341 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 390

RESULT 9
AA97173
ID AA97173 standard; protein; 525 AA.
XX AC AA97173;
XX DT 04-DEC-2000 (first entry)
XX DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 4.
XX KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
XX immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
XX inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnery;
XX ophthalmological; anti-proliferative.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX Peptide 1..21
FT /label= FGF-R1_signal_peptide
FT Domain 22..285
FT /label= FGF-R1_extracellular_domain
FT /note= "Ig I segment is deleted"
FT Domain 37..44
FT /label= Acid_box_segment
FT Domain 87..139
FT /label= Ig_II_segment
FT Peptide 286..293
FT /label= Linker
FT Region 294..525
FT /label= Human IgG1_Fc_region
FT /note= "Contains hinge region and domains CH2 and CH3"
FT Misc-difference 313

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FT /label= L313E
FT /note= "The mutation decreases the affinity of the Fc
FT portion for Fc receptors"
FT Misc-difference 409
FT /label= P409S
FT /note= "The mutation decreases the affinity of the Fc
FT portion for complement"
FT 445..250
FT /label= Ig_III_segment
XX
PN WO200046380-A2.
XX
XX 10-AUG-2000.
XX
XX 07-FEB-2000; 2000WO-US003166.
XX
XX 08-FEB-1999; 99US-0119002P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Kavanaugh WM, Ballinger M;
XX
XX WPI; 2000-514961/46.
XX
XX N-PSDB; AAA52130.
XX
XX New polypeptide comprising a fibroblast growth factor receptor
XX extracellular domain fused to a heterologous oligomerization domain for
XX treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX
XX Claim 14; Page 61-62; 70pp; English.
XX
XX Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
XX receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
XX (Ig) I segment fused to a heterologous oligomerization domain that
XX comprises an immunoglobulin FC region, hinge region, CH1, CH2, CH3 or CH4
XX region, or light chain of an immunoglobulin molecule, or a peptide with a
XX leucine zipper motif. The Ig I segment is not necessary for binding of
XX acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
XX affinity for aFGF and heparin, protects the core of the molecule from
XX proteolysis, and abrogates the heparin requirement for aFGF binding. The
XX new fusion polypeptides are better FGF inhibitors than FGF-R monomer
XX proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at
XX subnanomolar concentrations and were 20-fold more potent than the FGF-R
XX monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
XX fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
XX mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung,
XX rectal, testis and cervical tumours), neovascularization (e.g. diabetic
XX retinopathy, neovascular glaucoma, wound healing and corneal scarring)
XX and hyper-proliferation of vascular smooth muscle cells (e.g.
XX postangioplasty and postatherectomy restenosis)
XX
XX Sequence 525 AA;
XX
XX Query Match 95.7%; Score 562; DB 3; Length 525;
XX Best Local Similarity 95.5%; Pred. No. 2.7e-49;
XX Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
XX : |||||
XX 309 APELEGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 368
XX : |||||
XX
XX 61 PREEQYNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
XX : |||||
XX 369 PREEQYNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKALPASIEKTIKAK 418
XX : |||||
XX
XX RESULT 10
XX AAW85692
XX ID AAW85692 standard; protein; 711 AA.
XX
XX AC AAW85692;
XX
XX 12-AUG-1999 (first entry)

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XX MotAbII fusion protein.
XX
XX Antibody; humanised; variable region; heavy chain; light chain;
XX interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
XX immune disease; multiple sclerosis; Crohn's disease; skin disorders;
XX inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
XX multivalent; ruminant.
XX
XX Synthetic.
XX
XX Location/Qualifiers
XX Key 1..20
XX Peptide /label= Mouse_D9D10_light_chain_signal_peptide
XX Domain 21..137
XX /note= "Humanised heavy chain variable domain of D9D10"
XX Domain 138..467
XX /note= "Human IGG1 heavy chain constant domain"
XX Misc-difference 468
XX /note= "Leu added by cloning strategy"
XX Region 469..472
XX /label= Gly(3)Ser_linker
XX Domain 473..711
XX /label= Humanised_D9D10_ScFv
XX
XX WO9909055-A2.
XX
XX 25-FEB-1999.
XX
XX 14-AUG-1998; 98WO-EP005165.
XX
XX 18-AUG-1997; 97EP-00870122.
XX
XX 18-JUN-1998; 98EP-00870139.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Buyse M, Sablon E;
XX
XX WPI; 1999-180969/15.
XX
XX N-PSDB; AAW85692.
XX
XX New engineered antibodies which bind and neutralise interferon-gamma -
XX useful for prevention and treatment of septic shock, cachexia, immune
XX diseases and skin disorders.
XX
XX Disclosure; Fig 20; 134pp; English.
XX
XX New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
XX be used as a medicament, for preventing or treating septic shock, cachexia,
XX immune diseases including multiple sclerosis and Crohn's disease and skin
XX disorders including bullous, inflammatory and neoplastic dermatoses. The
XX antibody is selected from a single chain antibody (scFv), a chimeric
XX antibody or diabody comprising the humanised variable domain of the
XX monoclonal mouse anti-IFN gamma antibody D9D10; a multivalent antibody;
XX or a ruminant antibody. The antibodies are also useful for determining
XX IFN gamma levels in a sample
XX
XX Sequence 711 AA;
XX
XX Query Match 95.7%; Score 562; DB 2; Length 711;
XX Best Local Similarity 95.5%; Pred. No. 3.9e-49;
XX Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
XX : |||||
XX 251 APELLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
XX : |||||
XX
XX 61 PREEQYNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
XX : |||||
XX 311 PREEQYNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKALPASIEKTIKAK 360
XX : |||||
XX
XX RESULT 11

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CC constructed based on human immunoglobulin gammal protein (SEQ ID NO:6)  
 CC sequence shown in column 92-93 (AAE35214)  
 XX  
 SQ Sequence 251 AA;

Query Match 95.4%; Score 560; DB 6; Length 251;  
 Best Local Similarity 95.5%; Pred. No. 1.8e-49;  
 Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
 Db 35 APELLGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 Db 95 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 144

RESULT 13  
 ABB81492  
 ID ABB81492 standard; protein; 232 AA.  
 XX  
 AC ABB81492;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human mutated Fc protein designated Fc5 SEQ ID NO:32.  
 XX  
 KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;  
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;  
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;  
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;  
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;  
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;  
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;  
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;  
 KW light chain neuropathy; hypertension; large vessel disease;  
 KW graft-versus host disease; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200238766-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 XX 05-NOV-2001; 2001WO-US047018.  
 XX  
 XX 07-NOV-2000; 2000US-0246449P.  
 XX  
 XX 20-DEC-2000; 2000US-0257131P.  
 XX  
 XX 28-JUN-2001; 2001US-0301715P.  
 XX  
 XX 29-AUG-2001; 2001US-0315565P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Gross JA, Xu W, Henne RM, Grant FJ;  
 XX  
 XX WPI; 2002-508212/54.  
 XX  
 XX N-PSDB; ABN8947.  
 XX  
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed  
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage  
 PT renal failure or renal disease and lymphoma.  
 XX  
 XX Example 4; Page 148-149; 154pp; English.  
 XX  
 XX The present invention describes a human tumour necrosis factor receptor  
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,  
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive  
 CC activities, and can be used in gene therapy. (I) can be used for  
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12

(e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. Human Ztnfr12 is located to chromosome 22q13.2. The present sequence represents a mutated Fc protein designated Fc5, which is used in an example from the present invention

XX Sequence 232 AA;

Query Match 95.1%; Score 558; DB 5; Length 232;  
 Best Local Similarity 95.1%; Pred. No. 2.6e-49;  
 Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
 Db 16 APEAGAPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 Db 76 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 125

RESULT 14  
 ABB81491  
 ID ABB81491 standard; protein; 232 AA.  
 XX  
 AC ABB81491;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human mutated Fc designated Fc4 protein SEQ ID NO:28.  
 XX  
 KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;  
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;  
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;  
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;  
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;  
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;  
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;  
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;  
 KW light chain neuropathy; hypertension; large vessel disease;  
 KW graft-versus host disease; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200238766-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 XX 05-NOV-2001; 2001WO-US047018.  
 XX  
 XX 07-NOV-2000; 2000US-0246449P.  
 XX  
 XX 20-DEC-2000; 2000US-0257131P.  
 XX  
 XX 28-JUN-2001; 2001US-0301715P.  
 XX  
 XX 29-AUG-2001; 2001US-0315565P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Gross JA, Xu W, Henne RM, Grant FJ;  
 XX  
 XX WPI; 2002-508212/54.  
 XX  
 XX N-PSDB; ABN8947.  
 XX  
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed  
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage  
 PT renal failure or renal disease and lymphoma.  
 XX  
 XX Example 4; Page 148-149; 154pp; English.  
 XX  
 XX The present invention describes a human tumour necrosis factor receptor  
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,  
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive  
 CC activities, and can be used in gene therapy. (I) can be used for  
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12



```

DR WPI; 2002-508212/54.
DR N-PSDB; AEN89444.
XX
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Znf12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
XX
XX Example 4; Page 146; 154pp; English.
XX
CC The present invention describes a human tumor necrosis factor receptor
CC designated Znf12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Znf12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. Human Znf12 is located to chromosome 22q13.2. The
CC present sequence represents a mutated Fc protein designated Fc4, which is
CC used in an example from the present invention
XX
XX Sequence 232 AA;
SQ
Query Match 95.1%; Score 558; DB 5; Length 232;
Best Local Similarity 95.5%; Pred. No. 2.6e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 16 APEAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 76 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 125
RESULT 15
AAE35220
ID AAE35220 standard; protein; 250 AA.
XX
XX AAE35220;
XX
XX
XX 28-MAY-2003 (first entry)
XX
XX Human modified immunoglobulin moiety #3.
XX
XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
XX TACT; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
XX anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
XX glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
XX dermatological; neuroprotective; cyclophilin ligand-interactor; human;
XX autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; rheumatoid arthritis; renal disease; inflammation.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200294852-A2.
XX
XX 28-NOV-2002.
XX
XX

```

20-MAY-2002; 2002WO-US015910.

24-MAY-2001; 2001US-0293343P.

(ZYMO ) ZYMOGENETICS INC.

Rixon MW, Gross JA;

WPI; 2003-148455/14.

N-PSDB; AAD53758.

Transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACT)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACT receptor group and an immunoglobulin group.

Disclosure; Col 110-111; 71pp; English.

The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACT) receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or ZTNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is human modified immunoglobulin moiety used in the invention

Sequence 250 AA;

Query Match 95.1%; Score 558; DB 6; Length 250;

Best Local Similarity 95.5%; Pred. No. 2.8e-49;

Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 35 APEAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94

Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

Db 95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 144

Search completed: November 17, 2005, 07:04:55

Job time : 92.6667 secs



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	557	94.9	234	2	PT0207	Ig gamma chain C r
2	557	94.9	255	4	S31866	Ig gamma-1 chain C
3	557	94.9	330	1	GHHU	Ig gamma-1 chain C
4	557	94.9	374	2	S69339	Ig heavy chain V r
5	553	94.2	327	1	G4HU	Ig gamma-4 chain C
6	543.5	92.6	327	1	G2HU	Ig gamma-2 chain C
7	539	91.8	376	2	A23511	Ig gamma-3 chain C
8	539	91.8	377	2	A60764	Ig gamma-3 chain C
9	539	88.4	289	1	G3HUW1	Ig gamma-3 heavy c
10	458	78.0	328	2	I47160	Ig gamma-2b chain
11	458	78.0	328	2	I47159	Ig gamma-2a chain
12	453	77.2	327	2	I47162	Ig gamma-4 chain c
13	440	75.0	470	2	S22080	Ig heavy chain pre
14	434	73.9	328	2	I47161	Ig gamma-3 chain c
15	434	73.9	328	2	I47158	Ig gamma-1 chain c
16	431	73.4	333	2	PS0018	Ig gamma-2b chain
17	421	71.7	308	2	C30554	Ig heavy chain C r
18	421	71.7	323	1	GHRB	Ig gamma-2 chain C
19	421	71.7	329	1	G2GP	Ig gamma-2 chain C
20	421	71.7	472	2	S31459	Ig gamma-1 chain
21	418	71.2	329	1	G3MSC	Ig gamma-3 chain C
22	418	71.2	398	1	G3MSM	Ig gamma-3 chain C
23	410	69.8	327	2	S06611	Ig gamma-2 chain C
24	397	67.6	405	1	G2MSBM	Ig gamma-2b chain
25	397	67.6	474	1	G2MS11	Ig gamma-2b chain
26	396	67.5	324	1	G1NS	Ig gamma-1 chain C
27	396	67.5	329	2	S00847	Ig gamma-2c chain
28	396	67.5	393	1	G1NSM	Ig gamma-1 chain C
29	396	67.5	444	2	PC4436	monoclonal antibody

Best Local Similarity	94.5%;	Pred. No. 1.5e-47;
Matches 104;	Conservative	2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
| : |||||  
Db 39 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98  
| : |||||  
QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110  
| : |||||  
Db 99 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKALPAPIEKTISKAK 148  
| : |||||

RESULT 3  
GHU  
Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:62274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>  
A:Cross-references: UNIPROT:P01857; EMBL:Z17370  
A:Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers,  
A:Note: Lys-330 is removed after translation  
R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S33904  
A:Accession: S36861  
A:Molecule type: DNA  
A:Residues: 2-330 <HAR>  
A:Cross-references: EMBL:Z17370  
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A:Reference number: S33887; MUID:83001943; PMID:6811139  
A:Accession: S33887  
A:Molecule type: DNA  
A:Residues: 88-113;235-330 <TAK>  
A:Cross-references: EMBL:Z17370  
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
Biochemistry 9, 3161-3170, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A:Reference number: A90563; MUID:71064024; PMID:5489771  
A:Contents: myeloma protein Eu  
A:Accession: B90563  
A:Molecule type: Protein  
A:Residues: 1-96, R',98-135 <GUN>  
A:Note: this sequence has the Gm(3) marker, 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ  
A:Reference number: A90564; MUID:71064025; PMID:5530842  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: Protein  
A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,  
A:Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1504, 1976  
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
A:Note: this sequence has the Gm(17) and Gm(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI  
A:Reference number: A91723; MUID:83289131; PMID:6884994

A:Contents: myeloma protein KOI; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH:  
A:Note: this sequence has the Gm(3) and Gm(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMI>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 94.9%; Score 557; DB 1; Length 330;  
Best Local Similarity 94.5%; Pred. No. 2.1e-47;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
| : |||||  
Db 114 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173  
| : |||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110  
| : |||||  
Db 174 PREEQYNSTYRVVSVLTVTLQHDWLNGKEYKCKVSNKALPAPIEKTISKAK 223  
| : |||||

RESULT 4  
S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamlichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140,'C',142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 94.9%; Score 557; DB 2; Length 374;  
Best Local Similarity 94.5%; Pred. No. 2.4e-47;

A;Reference number: A93906; MUID:82197621; PMID:6804948  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <ELL>  
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A;Reference number: A92809; MUID:81007873; PMID:6774012  
A;Contents: myeloma protein Til  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a  
A;Reference number: A90752; MUID:80001357; PMID:113060  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24,'E',26-57,'EV',60-85:132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-  
A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g  
A;Reference number: A93132; MUID:80114419; PMID:118920  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati  
ned  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500; PMID:4940472  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124; PMID:5782707  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG2  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 14q32.33-14q32.33  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;133-202/Domain: immunoglobulin homology <IM2>  
F;239-306/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83,140-200,246-304/Disulfide bonds: #status experimental  
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;176/Binding site: carbohydrate (Asn) #status predicted

Query Match 92.6%, Score 543.5, DB 1; Length 326;  
Best Local Similarity 92.7%; Pred. No. 4.4e-46;  
Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
QY 1 APPVAGPSVFLPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 111 APPVA-GPSVFLPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 169  
QY 61 PREEQYNSTYRVVSVLTVTLVHDLWNLNGKEYCKCKVSNKGLPSSIEKTIKAK 110

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK 110





Search completed: November 17, 2005, 07:11:37  
Job time : 18.0822 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 80.6164 Seconds  
(without alignments)  
698.725 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSVFLFPFKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	94.9	330	1 GCL HUMAN	P01857 homo sapien
2	557	94.9	348	2 Q6PYX1	Q6PYX1 homo sapien
3	557	94.9	465	2 Q6GMX6	Q6GMX6 homo sapien
4	557	94.9	466	2 Q6IN78	Q6IN78 homo sapien
5	557	94.9	469	2 Q7Z7P5	Q7Z7P5 homo sapien
6	557	94.9	469	2 Q7Z7P5	Q7Z7P5 homo sapien
7	557	94.9	470	2 Q6PJ44	Q6PJ44 homo sapien
8	557	94.9	470	2 Q7Z5W1	Q7Z5W1 homo sapien
9	557	94.9	472	2 Q6N089	Q6N089 homo sapien
10	557	94.9	473	2 Q6MZV7	Q6MZV7 homo sapien
11	557	94.9	473	2 Q6P055	Q6P055 homo sapien
12	557	94.9	475	2 Q6GMW7	Q6GMW7 homo sapien
13	557	94.9	475	2 Q6MZ06	Q6MZ06 homo sapien
14	557	94.9	475	2 Q6N095	Q6N095 homo sapien
15	557	94.9	476	2 Q6GMX1	Q6GMX1 homo sapien
16	557	94.9	478	2 Q6PI81	Q6PI81 homo sapien
17	557	94.9	480	2 Q6N094	Q6N094 homo sapien
18	557	94.9	480	2 Q6PJF1	Q6PJF1 homo sapien
19	557	94.9	481	2 Q6N097	Q6N097 homo sapien
20	557	94.9	482	2 Q7Z351	Q7Z351 homo sapien
21	557	94.9	544	2 Q6PJ95	Q6PJ95 homo sapien
22	554	94.4	466	2 Q6N096	Q6N096 homo sapien
23	553	94.2	327	1 G4 HUMAN	P01861 homo sapien
24	553	94.2	473	2 Q8TC63	Q8TC63 mus sp. fv/
25	552	94.0	487	2 Q6MZL2	Q6MZL2 mus sp. fv/
26	550	93.7	476	2 Q6MZK7	Q6MZK7 homo sapien
27	543.5	92.6	327	1 GCL HUMAN	P01859 homo sapien
28	543.5	92.6	417	2 Q6N093	Q6N093 homo sapien
29	543.5	92.6	465	2 Q6P6C4	Q6P6C4 homo sapien
30	540.5	92.1	464	2 Q6MZU6	Q6MZU6 homo sapien
31	539	91.8	354	2 Q86TT2	Q86TT2 homo sapien

## RESULT 1

ID	GCL HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	IG gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RN	Biochemistry 9:3161-3170(1970).			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RN	Biochemistry 9:3171-3181(1970).			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			

32	539	91.8	518	2	Q6N030	Q6N030 homo sapien
33	535	91.1	509	2	Q8NF17	Q8NF17 homo sapien
34	535	91.1	521	2	Q8N4Y9	Q8N4Y9 homo sapien
35	534.5	91.1	493	2	Q68CN4	Q68CN4 homo sapien
36	519	88.4	290	1	GC3 HUMAN	P01860 homo sapien
37	458	78.0	337	2	Q95M34	Q95M34 equus caball
38	431	73.4	333	1	GCB_RAT	P20761 rattus norv
39	421	71.7	323	1	GC_RABIT	P01870 oryctolagus
40	421	71.7	329	1	GC2_CAVPO	P01862 cavia porce
41	418	71.2	303	2	Q6KAM2	Q6KAM2 mus musculu
42	418	71.2	329	1	GC3_MOUSE	P22436 mus musculu
43	418	71.2	398	1	GC3M_MOUSE	P03987 mus musculu
44	418	71.2	470	2	Q7TMK1	Q7TMK1 mus musculu
45	397	67.6	336	1	GCB_MOUSE	P01866 mus musculu

## ALIGNMENTS

RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RP Biochemistry 9:3188-3196(1970).  
 RP [7]  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from *Staphylococcus*  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -!- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC GIM(3) marker and the GLM (non-1) markers.  
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
 DR PIR; A93433; GHU.  
 DR PDB; 1AJ7; X-ray; H=1-103.  
 DR PDB; 1D5B; X-ray; B/H=1-101.  
 DR PDB; 1D5I; X-ray; H=1-101.  
 DR PDB; 1D6V; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1E4K; X-ray; A/B=106-329.  
 DR PDB; 1FC1; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCC; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I7Z; X-ray; B/D=1-103.  
 DR PDB; 1IIS; X-ray; A/B=107-330.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1OXX; X-ray; A/B=119-330.  
 DR PDB; 2RCS; X-ray; H=1-103.  
 DR Genew; HGNC:5525; IGHG1.  
 DR MIM; 147100; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW immunoglobulin C region; Immunoglobulin domain.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT HINGE 99 110

FT	DOMAIN	111	223	CH2.
FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	
FT	DISULFID	103	103	Interchain (with light chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	N-linked (GlcNAc, -).
FT	VARIANT	97	97	K -> R (in GIM(3) marker).
FT				/FTid=VAR_003886.
FT				D -> E (in GIM(non-1) marker).
FT	VARIANT	239	239	/FTid=VAR_003887.
FT				L -> M (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTid=VAR_003888.
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	STRAND	176	177	
FT	TURN	179	180	
FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	TURN	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EB106C2FA33D CRC64;

Query Match 94.9%; Score 557; DB 1; Length 330;  
 Best Local Similarity 94.5%; Pred. No. 3.5e-47;  
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
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 DB 114 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173





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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.CI.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGCI; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDE81076E CRC64;

Query Match 94.9%; Score 557; DB 2; Length 466;
Best Local Similarity 94.5%; Pred. No. 5.2e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 250 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 309

Qy 61 PREEQYNSTYRVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 310 PREEQYNSTYRVSVLTVHLQDWLNGKEYCKVSNKALPAIEKTIKAK 359

RESULT 5
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.CI.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 94.9%; Score 557; DB 2; Length 469;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 253 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 312

Qy 61 PREEQYNSTYRVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 313 PREEQYNSTYRVSVLTVHLQDWLNGKEYCKVSNKALPAIEKTIKAK 362

RESULT 6
Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; IG; 2.
DR SMART; SM00406; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 470;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db ||:|||||
254 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db ||:|||||
314 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETIKAK 363

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AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;

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RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 94.9%; Score 557; DB 2; Length 470;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db ||:|||||
254 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db ||:|||||
314 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETIKAK 363

RESULT 8
Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 472;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db ||:|||||
256 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 315

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db ||:|||||

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Db 316 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 365

RESULT 9

Q6MZV7 PRELIMINARY; PRT; 473 AA.

AC Q6MZV7;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686C11235.

GN Name=DKFZp686C11235;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RP TISSUE=Human small intestine;

RG The German Human cDNA Consortium;

RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

RA Fobo G., Han M., Wiemann S.;

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

EMBL; BX640853; CAB45920.1; -.

DR HSP; P01861; IADQ.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_cl.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; Ig; 2.

DR SMART; SM00407; IGL; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG MHC; UNKNOWN 2.

DR KW Hypothetical protein.

Q6MZV7 SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BF447 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 473;

Best Local Similarity 94.5%; Pred. No. 5.3e-47;

Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSGSVLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 257 APELLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 316

Qy 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK 110

Db 317 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 366

RESULT 10

Q6P055 PRELIMINARY; PRT; 473 AA.

AC Q6P055;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RP TISSUE=Peripheral Nervous System;

RG MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1F55D736860F8 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPAPIEKTISKAK 368

RESULT 12
Q6MZQ6
ID Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAB45972.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPAPIEKTISKAK 368

RESULT 14
Q6GNX1

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DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAB255A26F4B8E CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPAPIEKTISKAK 368

RESULT 13
Q6N095
ID Q6N095 PRELIMINARY; PRT; 475 AA.
AC Q6N095;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686K03196.
GN Name=DKFZp686K03196;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640821; CAB45775.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 475;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 259 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 318
Qy 61 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPSSIEKTIKAK 110
Db 319 PREEQYNSTYRVSVLTVLHODWLNKGKEYCKVKNKGLPAPIEKTISKAK 368

RESULT 14
Q6GNX1

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Thu Nov 17 11:27:21 2005

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ID O6GMX1 PRELIMINARY; PRT; 476 AA.
AC O6GMX1; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH3773.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 94.9%; Score 557; DB 2; Length 476;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 260 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 319
OY 61 PREEQNSTYRYVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 320 PREEQNSTYRYVSVLTVLHQLDNLNGKEYCKVSNKGLPAPIEKTSKAK 369

RESULT 15
Q6P181 PRELIMINARY; PRT; 478 AA.
AC Q6P181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 94.9%; Score 557; DB 2; Length 478;
Best Local Similarity 94.5%; Pred. No. 5.4e-47;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 262 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 321
OY 61 PREEQNSTYRYVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 322 PREEQNSTYRYVSVLTVLHQLDNLNGKEYCKVSNKGLPAPIEKTSKAK 371

Search completed: November 17, 2005, 07:10:20
JOB time : 81.6164 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:51:22 ; Search time 24.6119 Seconds  
(without alignments)  
333.636 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVFLPPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	97.1	447	4	US-09-968-362A-22
2	562	95.7	468	3	US-09-485-737B-67
3	562	95.7	468	4	US-10-071-485-67
4	562	95.7	488	4	US-09-499-846-12
5	562	95.7	497	4	US-09-499-846-10
6	562	95.7	525	4	US-09-499-846-8
7	562	95.7	711	3	US-09-485-737B-90
8	562	95.7	711	4	US-10-071-485-90
9	558	95.1	449	4	US-09-968-362A-20
10	558	95.1	559	4	US-09-746-359A-62
11	558	95.1	594	4	US-09-746-359A-23
12	557	94.9	110	3	US-08-444-644-21
13	557	94.9	110	3	US-08-232-246A-21
14	557	94.9	116	2	US-08-232-539D-55
15	557	94.9	212	1	US-08-430-633-4
16	557	94.9	212	2	US-08-620-694A-4
17	557	94.9	212	2	US-08-936-854-4
18	557	94.9	212	3	US-09-022-255-4
19	557	94.9	212	3	US-09-022-696-4
20	557	94.9	212	3	US-09-022-253-4
21	557	94.9	212	3	US-09-022-260-4
22	557	94.9	212	3	US-09-022-259-4
23	557	94.9	212	3	US-09-022-257-4
24	557	94.9	212	4	US-09-549-679-4
25	557	94.9	212	4	US-10-033-522-2
26	557	94.9	218	4	US-09-483-588-3
27	557	94.9	218	4	US-09-483-588-4

28	557	94.9	228	4	US-09-428-082B-2	Sequence 2, Appli
29	557	94.9	228	4	US-09-847-249A-2	Sequence 2, Appli
30	557	94.9	228	4	US-09-840-669B-2	Sequence 2, Appli
31	557	94.9	228	4	US-09-843-221A-2	Sequence 2, Appli
32	557	94.9	228	4	US-09-709-704A-2	Sequence 2, Appli
33	557	94.9	228	4	US-09-422-838C-5	Sequence 5, Appli
34	557	94.9	229	4	US-09-122-144-2	Sequence 2, Appli
35	557	94.9	232	2	US-08-595-043A-50	Sequence 50, Appli
36	557	94.9	232	4	US-09-968-362A-26	Sequence 26, Appli
37	557	94.9	235	3	US-09-131-247-6	Sequence 6, Appli
38	557	94.9	235	4	US-09-784-623-6	Sequence 6, Appli
39	557	94.9	243	4	US-09-428-082B-1068	Sequence 1068, Ap
40	557	94.9	247	4	US-09-428-082B-6	Sequence 6, Appli
41	557	94.9	247	4	US-09-428-082B-12	Sequence 12, Appli
42	557	94.9	248	4	US-09-428-082B-1056	Sequence 1056, Ap
43	557	94.9	248	4	US-09-428-082B-1058	Sequence 1058, Ap
44	557	94.9	248	4	US-09-428-082B-1060	Sequence 1060, Ap
45	557	94.9	248	4	US-09-428-082B-1062	Sequence 1062, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-968-362A-22  
; Sequence 22, Application US/09968362A  
; Patent No. 6797493  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulating factor  
; FILE REFERENCE: 03SUN2001  
; CURRENT APPLICATION NUMBER: US/09/968.362A  
; CURRENT FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 22  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hg-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2)  
; OTHER INFORMATION: C)  
US-09-968-362A-22

Query Match		97.1%;	Score 570;	DB 4;	Length 447;
Best Local Similarity		97.3%;	Pred. No. 3.9e-59;		
Matches 107;		Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	60		
Db	231	APEVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	290		
Qy	61	PREEQYNSTYRVSVLTVLHODNLNGKEYCKVSKNKGSLPSIEKTIKAK	110		
Db	291	PREEQYNSTYRVSVLTVLHODNLNGKEYCKVSKNKGSLPSIEKTIKAK	340		

##### RESULT 2

US-09-485-737B-67  
; Sequence 67, Application US/09485737B  
; Patent No. 6350860  
; GENERAL INFORMATION:  
; APPLICANT: Buysee, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
; FILE REFERENCE: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; CURRENT APPLICATION NUMBER: US/09/485.737B  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165

```

; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

Query Match          95.7%; Score 562; DB 3; Length 468;
Best Local Similarity 95.5%; Pred. No. 3.7e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 311 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 360

RESULT 3
US-10-071-485-67
; Sequence 67, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-67

Query Match          95.7%; Score 562; DB 4; Length 468;
Best Local Similarity 95.5%; Pred. No. 3.7e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 311 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPASTIEKTIKAK 360

RESULT 4
```

```

US-09-499-846-12
; Sequence 12, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-12

Query Match          95.7%; Score 562; DB 4; Length 488;
Best Local Similarity 95.5%; Pred. No. 3.9e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 272 APELGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 332 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPASTIEKTIKAK 381

RESULT 5
US-09-499-846-10
; Sequence 10, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-10

Query Match          95.7%; Score 562; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 4e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 281 APELGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 341 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPASTIEKTIKAK 390

RESULT 6
US-09-499-846-8
; Sequence 8, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-8

Query Match          95.7%; Score 562; DB 4; Length 497;
Best Local Similarity 95.5%; Pred. No. 4e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 281 APELGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 340

Qy 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 341 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPASTIEKTIKAK 390
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; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-8

Query Match          95.7%; Score 562; DB 4; Length 525;
Best Local Similarity 95.5%; Pred. No. 4.3e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   ||:|||||
Db 309 APELGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 368
   ||:|||||

Qy 61 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
   |||||||
Db 369 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 418
   |||||||

RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match          95.7%; Score 562; DB 3; Length 711;
Best Local Similarity 95.5%; Pred. No. 6.5e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   ||:|||||
Db 251 APELGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
   ||:|||||

Qy 61 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
   |||||||
Db 311 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 360
   |||||||

RESULT 8
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
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; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match          95.7%; Score 562; DB 4; Length 711;
Best Local Similarity 95.5%; Pred. No. 6.5e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   ||:|||||
Db 251 APELGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
   ||:|||||

Qy 61 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
   |||||||
Db 311 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 360
   |||||||

RESULT 9
US-09-968-362A-20
; Sequence 20, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2
; OTHER INFORMATION: B)
US-09-968-362A-20

Query Match          95.1%; Score 558; DB 4; Length 449;
Best Local Similarity 95.5%; Pred. No. 1e-57;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   |||||||
Db 233 APEFAGGSPVFLPPPKDQTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
   |||||||

Qy 61 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
   |||||||
Db 293 PREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 342
   |||||||

RESULT 10
US-09-746-359A-62
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Best Local Similarity 94.5%; Pred. No. 2.1e-58;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
|| : |||||  
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110  
|| : |||||

RESULT 13  
US-08-232-246A-21  
; Sequence 21, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Frigen, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232.246A  
; FILING DATE: 04-MAY-1994

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989

ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-232-246A-21

Query Match 94.9%; Score 557; DB 3; Length 110;  
Best Local Similarity 94.5%; Pred. No. 2.1e-58;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
|| : |||||  
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110  
|| : |||||

RESULT 14  
US-08-232-539D-55  
; Sequence 55, Application US/08232539D  
; Patent No. 5965709  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Ige Antagonists  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232.539D  
; FILING DATE: 21-Apr-1994

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/178583  
; FILING DATE: 07-JAN-1994

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P3

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-232-539D-55

Query Match 94.9%; Score 557; DB 2; Length 116;  
Best Local Similarity 94.5%; Pred. No. 2.2e-58;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
Db 6 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65  
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
|| : |||||  
Db 66 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 115  
|| : |||||

RESULT 15  
US-08-430-633-4  
; Sequence 4, Application US/08430633  
; Patent No. 5726286  
; GENERAL INFORMATION:  
; APPLICANT: ALDERSON, MARK  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: COHEN, JEFFREY  
; APPLICANT: COMEAU, MICHAEL  
; APPLICANT: FARRAH, THERESA  
; APPLICANT: SPRIGGS, MELANIE  
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins  
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:

Thu Nov 17 11:27:20 2005

ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,633  
FILING DATE: 28-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/235,397  
FILING DATE: 04/28/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2612  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 212 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Human  
IMMEDIATE SOURCE:  
CLONE: IgG1 Fc  
US-08-430-633-4

Query Match 94.9%; Score 557; DB 1; Length 212;  
Best Local Similarity 94.5%; Pred. No. 5e-58;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 APPVAGGSPVLPFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
||:|||||  
Db 14 APELLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73  
Qy 61 PREEQYNSTYRVWSVLTVLVHODWLNKGEYCKVSNKGLPSSIEKTIISKAK 110  
|||:|||||  
Db 74 PREEQYNSTYRVWSVLTVLVHODWLNKGEYCKVSNKGLPAPIEKTIISKAK 123

Search completed: November 17, 2005, 07:13:22  
Job time : 25.6119 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:05:08 ; Search time 84.3836 Seconds  
(without alignments)  
545.427 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGPSVFLFPKPKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	98.6	110	18	US-10-959-318-9
2	579	98.6	110	18	US-10-959-318-10
3	570.5	97.2	329	20	US-11-102-403-25
4	570	97.1	435	10	US-09-932-812-22
5	570	97.1	435	16	US-10-761-593A-22
6	570	97.1	435	20	US-11-016-518A-22
7	570	97.1	435	20	US-11-017-185-22
8	570	97.1	447	10	US-09-968-362-22
9	570	97.1	447	16	US-10-800-497-22
10	570	97.1	447	16	US-10-800-449-22
11	565	96.3	110	18	US-10-959-318-13
					Sequence 9, Appli
					Sequence 10, Appl
					Sequence 25, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 13, Appl

12	565	96.3	110	18	US-10-959-318-14	Sequence 14, Appl
13	563	95.9	110	18	US-10-959-318-7	Sequence 7, Appli
14	563	95.9	110	18	US-10-959-318-8	Sequence 8, Appli
15	562.5	95.8	109	18	US-10-959-318-11	Sequence 11, Appl
16	562.5	95.8	109	18	US-10-959-318-12	Sequence 12, Appl
17	562	95.7	468	14	US-10-071-485-67	Sequence 67, Appl
18	562	95.7	468	18	US-10-685-581-67	Sequence 67, Appl
19	562	95.7	488	15	US-10-683-255-12	Sequence 12, Appl
20	562	95.7	497	15	US-10-683-255-10	Sequence 10, Appl
21	562	95.7	500	18	US-10-627-556-274	Sequence 274, App
22	562	95.7	500	18	US-10-627-556-276	Sequence 276, App
23	562	95.7	525	15	US-10-683-255-8	Sequence 8, Appli
24	562	95.7	711	14	US-10-071-485-90	Sequence 90, Appl
25	562	95.7	711	18	US-10-985-581-90	Sequence 90, Appl
26	561	95.6	110	20	US-11-018-102-23	Sequence 23, Appl
27	561	95.6	330	17	US-10-706-689-3	Sequence 3, Appli
28	561	95.6	330	18	US-10-988-360-3	Sequence 3, Appli
29	561	95.6	330	20	US-11-102-403-26	Sequence 26, Appl
30	561	95.6	447	15	US-10-474-832-6	Sequence 6, Appli
31	560	95.4	227	17	US-10-822-231-124	Sequence 124, App
32	560	95.4	227	17	US-10-822-231-281	Sequence 281, App
33	559	95.2	110	20	US-11-018-102-25	Sequence 25, Appl
34	559	95.2	227	17	US-10-822-231-123	Sequence 123, App
35	559	95.2	227	17	US-10-822-231-127	Sequence 127, App
36	558	95.1	109	18	US-10-627-556-270	Sequence 270, App
37	558	95.1	216	18	US-10-627-556-272	Sequence 272, App
38	558	95.1	227	17	US-10-822-231-130	Sequence 130, App
39	558	95.1	227	17	US-10-822-231-134	Sequence 134, App
40	558	95.1	227	17	US-10-822-231-296	Sequence 296, App
41	558	95.1	232	14	US-10-008-063-28	Sequence 28, Appl
42	558	95.1	232	14	US-10-008-063-32	Sequence 32, Appl
43	558	95.1	250	14	US-10-152-363A-35	Sequence 35, Appl
44	558	95.1	251	14	US-10-152-363A-31	Sequence 31, Appl
45	558	95.1	251	14	US-10-152-363A-33	Sequence 33, Appl

#### ALIGNMENTS

RESULT 1  
US-10-959-318-9  
; Sequence 9, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; APPLICANT: Clark, Michael R  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)  
US-10-959-318-9

Query Match 98.6%; Score 579; DB 18; Length 110;  
Best Local Similarity 95.1%; Pred. No. 1.1e-48;  
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

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Qy 61 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110
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Db 61 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110

RESULT 2
US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and e (E269)
US-10-959-318-10

Query Match 98.6%; Score 579; DB 18; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.1e-48;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Qy 61 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110
      |||
Db 61 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110

RESULT 3
US-11-102-403-25
; Sequence 25, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PABEN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STUBENRAUCH, PAMELA
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 25
; LENGTH: 329
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-102-403-25

Query Match 97.2%; Score 570.5; DB 20; Length 329;
Best Local Similarity 99.1%; Pred. No. 2.5e-47;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
Db 114 APPVA-GPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 172

Qy 61 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110
      |||
Db 173 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 222

RESULT 4
US-09-932-812-22
; Sequence 22, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of human erythropoietin with increased biological activity
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2C)
US-09-932-812-22

Query Match 97.1%; Score 570; DB 10; Length 435;
Best Local Similarity 97.3%; Pred. No. 3.8e-47;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
Db 219 APEVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278

Qy 61 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110
      |||
Db 279 PREEQYNSTYRVSVSLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 328

RESULT 5
US-10-761-593A-22
; Sequence 22, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: FC fusion proteins of human erythropoietin with high biological activity
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2C)  
US-10-761-593A-22

Query Match 97.1%; Score 570; DB 16; Length 435;  
Best Local Similarity 97.3%; Pred. No. 3.8e-47;  
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 219 APEVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 279 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPASIEKTIKAK 328

## RESULT 6

US-11-016-518A-22  
Sequence 22, Application US/11016518A  
Publication No. US20050124045A1  
GENERAL INFORMATION:  
APPLICANT: Sun, Lee-Hwei K  
APPLICANT: Sun, Bill N  
APPLICANT: Sun, Cecily R  
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased  
TITLE OF INVENTION: Biological activities  
FILE REFERENCE: 02SUN2004D1  
CURRENT APPLICATION NUMBER: US/11/016,518A  
CURRENT FILING DATE: 2004-12-17  
PRIOR APPLICATION NUMBER: US 09/932,812  
PRIOR FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 22  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2C)  
US-11-016-518A-22

Query Match 97.1%; Score 570; DB 20; Length 435;  
Best Local Similarity 97.3%; Pred. No. 3.8e-47;  
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 219 APEVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 279 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPASIEKTIKAK 328

## RESULT 7

US-11-017-185-22  
Sequence 22, Application US/11017185  
Publication No. US20050142642A1  
GENERAL INFORMATION:  
APPLICANT: Sun, Lee-Hwei K  
APPLICANT: Sun, Bill N  
APPLICANT: Sun, Cecily R  
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological  
TITLE OF INVENTION: activities  
FILE REFERENCE: 02SUN2001D2  
CURRENT APPLICATION NUMBER: US/11/017,185  
CURRENT FILING DATE: 2004-12-17  
PRIOR APPLICATION NUMBER: US 09/932,812  
PRIOR FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 22  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2C)  
US-11-017-185-22

Query Match 97.1%; Score 570; DB 20; Length 435;  
Best Local Similarity 97.3%; Pred. No. 3.8e-47;  
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 219 APEVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 279 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPASIEKTIKAK 328

## RESULT 8

US-09-968-362-22  
Sequence 22, Application US/09968362  
Publication No. US20030082679A1  
GENERAL INFORMATION:  
APPLICANT: Sun, Lee-Hwei K  
APPLICANT: Sun, Bill N  
APPLICANT: Sun, Cecily R  
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
TITLE OF INVENTION: Biological activities  
FILE REFERENCE: 03SUN2001  
CURRENT APPLICATION NUMBER: US/09/968,362  
CURRENT FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 447  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2C)  
US-09-968-362-22

Query Match 97.1%; Score 570; DB 10; Length 447;  
Best Local Similarity 97.3%; Pred. No. 3.9e-47;  
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 APPVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 231 APEVAGGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPASIEKTIKAK 340

## RESULT 9

US-10-800-497-22  
Sequence 22, Application US/10800497  
Publication No. US20040259209A1  
GENERAL INFORMATION:  
APPLICANT: Sun, Lee-Hwei K  
APPLICANT: Sun, Bill N  
APPLICANT: Sun, Cecily R  
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor with  
TITLE OF INVENTION: increased biological activities  
FILE REFERENCE: 03SUN2001  
CURRENT APPLICATION NUMBER: US/10/800,497  
CURRENT FILING DATE: 2004-03-15

;; PRIOR APPLICATION NUMBER: US/09/968,362  
;; PRIOR FILING DATE: 2001-10-01  
;; NUMBER OF SEQ ID NOS: 28  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 22  
;; LENGTH: 447  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide  
;; OTHER INFORMATION: (Figure 2  
;; OTHER INFORMATION: C)  
US-10-800-497-22

Query Match 97.1%; Score 570; DB 16; Length 447;  
Best Local Similarity 97.3%; Pred. No. 3.9e-47;  
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
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Db 231 APEVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290  
|||  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
|||  
Db 291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 340  
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RESULT 10  
US-10-800-449-22  
;; Sequence 22, Application US/10800449  
;; Publication No. US20040265973A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sun, Lee-Hwei K  
;; APPLICANT: Sun, Bill  
;; APPLICANT: Sun, Cecily R  
;; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor  
;; FILE REFERENCE: increased biological activities  
;; TITLE OF INVENTION: 03SUN2001  
;; CURRENT APPLICATION NUMBER: US/10/800,449  
;; CURRENT FILING DATE: 2004-03-15  
;; PRIOR APPLICATION NUMBER: US/09/968,362  
;; PRIOR FILING DATE: 2001-10-01  
;; NUMBER OF SEQ ID NOS: 28  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 22  
;; LENGTH: 447  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2  
;; OTHER INFORMATION: C)  
US-10-800-449-22

Query Match 97.1%; Score 570; DB 16; Length 447;  
Best Local Similarity 97.3%; Pred. No. 3.9e-47;  
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|||  
Db 231 APEVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290  
|||  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
|||  
Db 291 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 340  
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RESULT 11  
US-10-959-318-13  
;; Sequence 13, Application US/10959318  
;; Publication No. US20050215768A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Armour, Kathryn L  
;; APPLICANT: Clark, Michael R

;; TITLE OF INVENTION: Polypeptides including modified constant regions  
;; FILE REFERENCE: 39-302  
;; CURRENT APPLICATION NUMBER: US/10/959,318  
;; CURRENT FILING DATE: 2004-10-07  
;; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
;; PRIOR FILING DATE: 2004-10-07  
;; PRIOR APPLICATION NUMBER: GB0324368.0  
;; PRIOR FILING DATE: 2003-10-17  
;; NUMBER OF SEQ ID NOS: 27  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 13  
;; LENGTH: 110  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)  
;; OTHER INFORMATION: mutations  
US-10-959-318-13

Query Match 96.3%; Score 565; DB 18; Length 110;  
Best Local Similarity 96.4%; Pred. No. 2.4e-47;  
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|||  
Db 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|||  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
|||  
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
|||

RESULT 12  
US-10-959-318-14  
;; Sequence 14, Application US/10959318  
;; Publication No. US20050215768A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Armour, Kathryn L  
;; APPLICANT: Clark, Michael R  
;; TITLE OF INVENTION: Polypeptides including modified constant regions  
;; FILE REFERENCE: 39-302  
;; CURRENT APPLICATION NUMBER: US/10/959,318  
;; CURRENT FILING DATE: 2004-10-07  
;; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
;; PRIOR FILING DATE: 2004-10-07  
;; PRIOR APPLICATION NUMBER: GB0324368.0  
;; PRIOR FILING DATE: 2003-10-17  
;; NUMBER OF SEQ ID NOS: 27  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 14  
;; LENGTH: 110  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268)  
;; OTHER INFORMATION: mutations  
US-10-959-318-14

Query Match 96.3%; Score 565; DB 18; Length 110;  
Best Local Similarity 96.4%; Pred. No. 2.4e-47;  
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|||  
Db 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|||  
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
|||  
Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
|||

RESULT 13  
US-10-959-318-7



; Sequence 7, Application US/10959318  
; Publication No. US20050215768A1

## GENERAL INFORMATION:

; APPLICANT: Armour, Kathryn L  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)  
; OTHER INFORMATION: mutations  
US-10-959-318-7

Query Match 95.9%; Score 563; DB 18; Length 110;

Best Local Similarity 96.4%; Pred. No. 3.8e-47;  
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Oy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

Db 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

## RESULT 14

US-10-959-318-8

; Sequence 8, Application US/10959318

; Publication No. US20050215768A1

## GENERAL INFORMATION:

; APPLICANT: Armour, Kathryn L  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and e (E268)  
; OTHER INFORMATION: mutations  
US-10-959-318-8

Query Match 95.9%; Score 563; DB 18; Length 110;

Best Local Similarity 96.4%; Pred. No. 3.8e-47;  
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Oy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

|||||

Db 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

## RESULT 15

US-10-959-318-11

; Sequence 11, Application US/10959318

; Publication No. US20050215768A1

## GENERAL INFORMATION:

; APPLICANT: Armour, Kathryn L  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)  
; OTHER INFORMATION: mutations  
US-10-959-318-11

Query Match 95.8%; Score 562.5; DB 18; Length 109;

Best Local Similarity 98.2%; Pred. No. 4.2e-47;  
Matches 108; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 1 APPVA-GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59

Oy 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

Db 60 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 109

Search completed: November 17, 2005, 07:37:36

Job time : 85.3836 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.9087 Seconds  
(without alignments)  
473.187 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APVAGGSRVFLPPKPKDT.....CKVSNKGLPSSIEKTIKRAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0  
Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	98.1	110	3 AAY54998	Mutated C
2	570.5	97.2	109	3 AAY54996	Mutated C
3	557	94.9	110	2 AAR27680	Human Imm
4	557	94.9	110	2 AAR41684	Human Imm
5	557	94.9	110	8 ADH75385	Human IgG
6	553	94.2	109	7 ADH25659	Binding d
7	553	94.2	110	2 AAR41717	Undefined
8	552	94.0	109	5 AAE28089	Human Imm
9	552	94.0	110	8 ADH75415	CH2 regio
10	551	93.9	110	8 ADL90103	Human Imm
11	550	93.7	110	8 ADH75413	CH2 regio
12	549	93.5	109	2 AAR67438	OKT3 mono
13	545	92.8	109	7 ADH25761	Binding d
14	543.5	92.6	109	2 AAR41709	Undefined
15	543.5	92.6	109	3 AAY54997	Mutated C
16	541	92.2	105	2 AAY42626	Human IgG
17	533	90.8	110	2 AAR41713	Undefined
18	528	89.9	102	8 ADJ52129	CH1 delet
19	526	89.6	102	8 ADJ52132	CH1 delet
20	415	70.7	110	2 AAW71023	Mus muscu
21	397	67.6	110	1 AAR83207	Sequence
22	357	60.8	72	8 ADL15711	Human Imm
23	344	58.6	66	2 AAR75349	C-gamma-1
24	344	58.6	66	2 AAR75351	C-gamma-1
25	318	54.2	76	8 ADL15713	Human Imm

26	286	48.7	56	1 AAR83204	Sequence
27	281	47.9	56	1 AAR83201	Sequence
28	281	47.9	56	1 AAR83203	Sequence
29	280	47.7	56	1 AAR83202	Sequence
30	275	46.8	56	1 AAR83206	Sequence
31	275	46.8	56	1 AAR83205	Sequence
32	249	42.4	46	8 AAR59138	Human IgG
33	234	39.9	46	8 AAR59139	Human IgG
34	232.5	39.6	110	2 AAR59142	Rhesus mo
35	221	37.6	46	8 AAR59143	Rhesus mo
36	215	36.6	46	8 AAR59140	Rhesus mo
37	209	35.6	46	8 AAR59141	Crab-eati
38	203.5	34.7	110	2 AAR59141	Variant I
39	201.5	34.3	110	2 AAR59141	Variant I
40	199	33.9	96	3 AAR59148	Human col
41	198	33.7	46	8 AAR59148	Human col
42	194	33.0	46	8 AAR59145	Pig IgG2a
43	193.5	33.0	110	2 AAR59147	Variant I
44	192	32.7	46	8 AAR59147	Llama IgG

## ALIGNMENTS

### RESULT 1

AAY54998

ID AAY54998 standard; protein; 110 AA.

XX AC AAY54998;

XX DT 17-FEB-2000 (first entry)

XX DE Mutated CH2 sequence G1deltaaac.

XX KW Binding molecule; CH2 sequence; complement dependent lysis; Fc gammaRIIb;

XX KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;

XX KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;

XX KW Crohn's disease; graft-vs-host disease; organ transplant rejection;

XX KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;

XX KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;

XX KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;

XX KW neonatal alloimmune thrombocytopenia; Goodpasture disease; therapy;

XX KW sickle cell anaemia; coronary artery occlusion.

XX OS Synthetic.

PN WO95958572-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001441.

XX PR 08-MAY-1998; 98GB-00009951.

XX XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX XX Armour KL, Clark MR, Williamson LM;

XX XX WPI; 2000-039075/03.

XX XX Immunoglobulin-derived binding molecules that do not activate complement

XX XX or trigger cytotoxic activities and maintaining desirable immunoglobulin

XX XX properties.

XX XX Claim 12; Fig 17; 81pp; English.

XX XX This sequence represents the mutated CH2 molecule G1deltaaac, and is a

XX XX binding molecule of the invention. The recombinant binding molecule is

XX XX capable of binding a target molecule without triggering complement

XX XX dependent lysis, or the cell-mediated destruction of the target

XX XX comprises: (a) a binding domain capable of binding a target molecule; and

XX XX (b) an effector domain that is homologous to all or part of a constant

CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
CC molecule is used to bind a target molecule (especially Fc gammaRIIb  
CC causing inhibition of B cell activation, mast cell degranulation or  
CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
CC binding of a second binding molecule, e.g. an antibody, to the target  
CC molecule. The binding molecule is useful for the treatment of graft-vs-  
CC host disease, organ transplant rejection, bone-marrow transplant  
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.  
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
CC coronary artery occlusion). The binding molecules do not activate  
CC complement or trigger cytotoxic activities through Fc gammaR and desirable  
CC Igg properties have been retained. The polypeptides do not contain non-  
CC human amino acids, and are therefore likely to have reduced  
CC immunogenicity. Further, they still bind Protein A, which is consistent  
CC with being able to cross the human placenta through interaction with FcRn  
CC (neonatal Fc receptor)  
XX  
SQ Sequence 110 AA;

Query Match 98.1%; Score 576; DB 3; Length 110;  
Best Local Similarity 99.1%; Pred. No. 1.4e-51;  
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
QY 61 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
DB 61 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 110

RESULT 2  
AA54996  
ID AA54996 standard; protein; 109 AA.  
XX  
AC AA54996;  
XX  
DT 17-FEB-2000 (first entry)  
XX  
DE Mutated CH2 sequence Gldeltaab.  
XX  
KW Binding molecule; CH2 sequence; complement dependent lysis; Fc gammaRIIb;  
KW cell-mediated destruction; human; immunoglobulin G; Igg heavy chain;  
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
KW sickle cell anaemia; coronary artery occlusion.  
XX  
OS Synthetic.  
XX  
FN WO9958572-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001441.  
XX  
PR 08-MAY-1998; 98GB-00009951.  
XX  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX  
XX Armour KL, Clark MR, Williamson LM;  
XX  
XX WPI; 2000-039075/03.  
XX  
PT Immunoglobulin-derived binding molecules that do not activate complement  
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin

PT properties.  
XX Claim 12; Fig 17; 81pp; English.  
PS  
XX  
CC This sequence represents the mutated CH2 molecule Gldeltaab, and is a  
CC binding molecule of the invention. The recombinant binding molecule is  
CC capable of binding a target molecule without triggering complement  
CC dependent lysis, or the cell-mediated destruction of the target  
CC comprises: (a) a binding domain capable of binding a target molecule; and  
CC (b) an effector domain that is homologous to all or part of a constant  
CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
CC molecule is used to bind a target molecule (especially Fc gammaRIIb  
CC causing inhibition of B cell activation, mast cell degranulation or  
CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
CC binding of a second binding molecule, e.g. an antibody, to the target  
CC molecule. The binding molecule is useful for the treatment of graft-vs-  
CC host disease, organ transplant rejection, bone-marrow transplant  
CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.  
CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
CC coronary artery occlusion). The binding molecules do not activate  
CC complement or trigger cytotoxic activities through Fc gammaR and desirable  
CC Igg properties have been retained. The polypeptides do not contain non-  
CC human amino acids, and are therefore likely to have reduced  
CC immunogenicity. Further, they still bind Protein A, which is consistent  
CC with being able to cross the human placenta through interaction with FcRn  
CC (neonatal Fc receptor)  
XX  
SQ Sequence 109 AA;

Query Match 97.2%; Score 570.5; DB 3; Length 109;  
Best Local Similarity 99.1%; Pred. No. 5.3e-51;  
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59  
QY 61 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 110  
DB 60 PREEQYNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 109  
RESULT 3  
AA27680  
ID AA27680 standard; protein; 110 AA.  
XX  
AC AA27680;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAR-1993 (first entry)  
XX  
DE Human immunoglobulin IgG1 CH2 region.  
XX  
KW Isoallotype; IgG1 G1m(1,2,17); anti-allotype response; humanised Ab.  
XX  
OS Homo sapiens.  
XX  
FN WO9216562-A1.  
XX  
PD 01-OCT-1992.  
XX  
PF 12-MAR-1992; 92WO-GB000445.  
XX  
PR 12-MAR-1991; 91GB-00005245.  
XX  
PA (LYNX-) LYNXVALE LTD.  
XX  
PI Clark MR;  
XX  
DR WPI; 1992-349162/42.

XX Humanised antibodies having modified allotypic determinant - useful for  
PT matching allotypes in therapy with decreased likelihood of causing  
PT undesirable immune responses.  
XX  
XX  
PS Disclosure; Fig 4c; 57pp; English.  
XX  
XX In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17.  
CC The inventor's propose eliminating these allotypes by amino acid changes  
CC to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype  
CC sites (1, 2 and 17) are located within the CH2 domain. New "isallotypes"  
CC should be suitable for therapeutic use in all patients. See AAR27678-  
CC R27681. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 110 AA;  
SQ

Query Match 94.9%; Score 557; DB 2; Length 110;  
Best Local Similarity 94.5%; Pred. No. 1.3e-49;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
DB 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110  
|| : |||||  
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110  
|| : |||||

RESULT 4  
AAR41684  
ID AAR41684 standard; protein; 110 AA.  
XX  
XX AAR41684;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT 20-OCT-1993 (first entry)  
DT  
XX  
XX Undefined ORF2 encoded by pAH4602.  
DE  
XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;  
KW chain; variable; constant; region; anti-human; transferrin; receptor;  
KW antibody; brain; capillary; endothelial cell; conjugate;  
KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy;  
KW Parkinsons disease; Alzheimers disease.  
XX  
XX Synthetic.  
OS  
XX WO9310819-A1.  
PN  
XX 10-JUN-1993.  
PD  
XX  
XX 24-NOV-1992; 92WO-US010206.  
PF  
XX  
XX 26-NOV-1991; 91US-00800458.  
PR  
XX  
XX (ALKE-) ALKERMES INC.  
PA  
XX  
XX Friden PM;  
PI  
XX  
XX WPI; 1993-196742/24.  
DR  
XX N-PSDB; AAQ43844.  
DR  
XX  
XX Antibody conjugates specific for transferrin receptor - used for  
PT diagnosis and treatment of cancer, AIDS and neurological disorders.  
PT  
XX  
XX Disclosure; Fig 11K; 151pp; English.  
PS  
XX The sequences given in AAR41682-85 are encoded by the expression vector,  
CC pAH4602. This vector contains open reading frames encoding the heavy  
CC chain variable region (VH) of the antibody 128.1, an ampicillin  
CC resistance gene and a histidine (histidinol) selection marker.  
CC  
XX Transcription of the VH gene is from the VH promoter of the murine 27.44

CC gene. The vector also includes a heavy chain immunoglobulin enhancer and  
CC the human gamma constant region (CH). The VH region of 128.1 was  
CC isolated by polymerase chain reaction and cloned into plasmid pAH4274.  
CC This was achieved by digesting the plasmid and the product with EcoRV and  
CC NheI. The VH gene was inserted in-frame with the human gamma1 CH region  
CC CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an  
CC anti-human transferrin receptor antibody which binds to the transferrin  
CC receptor on brain capillary endothelial cells. This antibody may be used  
CC in a conjugate in which it is linked to a neuro- pharmaceutical or  
CC diagnostic agent. The conjugate may be used to treat or prevent  
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 110 AA;  
SQ

Query Match 94.9%; Score 557; DB 2; Length 110;  
Best Local Similarity 94.5%; Pred. No. 1.3e-49;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
DB 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110  
|| : |||||  
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110  
|| : |||||

RESULT 5  
ADH75385  
ID ADH75385 standard; protein; 110 AA.  
XX  
XX ADH75385;  
AC  
XX  
XX 22-APR-2004 (first entry)  
DT  
XX  
XX Human IgG1 CH2 region.  
DE  
XX  
XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
KW autoimmune disease; human; IgG; immunoglobulin.  
KW  
XX Homo sapiens.  
OS  
XX US2004002587-A1.  
PN  
XX 01-JAN-2004.  
PD  
XX  
XX 20-FEB-2003; 2003US-00370749.  
PF  
XX  
XX 20-FEB-2002; 2002US-0358161P.  
PR  
XX  
XX (WATK/) WATKINS J D.  
PA (ALLA/) ALLAN B.  
PA  
XX  
XX Watkins JD, Allan B;  
PI  
XX  
XX WPI; 2004-070755/07.  
DR  
XX  
XX New composition comprising a variant of a parent polypeptide having at  
PT least a portion of a Fe region, useful in treating e.g., autoimmune  
PT diseases.  
XX  
XX Claim 20; SEQ ID NO 23; 62pp; English.  
PS  
XX The invention relates to a new composition comprises a variant of a  
CC parent polypeptide having at least a portion of a Fc region. The variant  
CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the  
CC presence of effector cells more effectively than the parent polypeptide  
CC and comprises at least one amino acid modification at position 280 in the  
CC Fc region. The composition is useful in treating diseases e.g.,  
CC autoimmune diseases. The present sequence represents the amino acid  
CC sequence of a human immunoglobulin G, IgG, CH region.

```
XX SQ Sequence 110 AA;
Query Match 94.9%; Score 557; DB 8; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.3e-49;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLFPPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 110

RESULT 6
ADD25659
ID ADD25659 standard; protein; 109 AA.
XX AC ADD25659;
XX DT 15-JAN-2004 (first entry)
XX DE Binding domain-immunoglobulin fusion protein-associated protein #107.
XX KW Binding domain; immunoglobulin; fusion protein; protein; cytostatic;
KW antithyroid; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type 1 diabetes mellitus; multiple sclerosis; autoimmune disease.
XX OS Unidentified.
XX PN US2003118592-A1.
XX PD 26-JUN-2003.
XX PF 25-JUL-2002; 2002US-00207655.
XX PR 17-JAN-2001; 2001US-0367358P.
XX PR 17-JAN-2002; 2002US-00053530.
XX PR 03-JUN-2002; 2002US-0385691P.
XX PA (GENE-) GENE-CRAFT INC.
XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX DR WPI; 2003-801317/75.
XX PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX PS Disclosure; SEQ ID NO 220; 157pp; English.
XX CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
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CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type 1 diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequences.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX SQ Sequence 109 AA;

Query Match 94.2%; Score 553; DB 7; Length 109;
Best Local Similarity 94.5%; Pred. No. 3.4e-49;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 PPVAGGSPVFLFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 1 PELLGGPSVFLFPPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

QY 62 REEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 REEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 109

RESULT 7
AAR41717
ID AAR41717 standard; protein; 110 AA.
XX AC AAR41717;
XX DT 25-MAR-2003 (revised)
XX DT 20-OCT-1993 (first entry)
XX DE Undefined ORF2 encoded by plasmid pAH4808.
XX KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
KW light; chain; variable; constant; region; anti-human; pAH4807;
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX OS Synthetic.
XX PN WO9310819-A1.
XX PD 10-JUN-1993.
XX PF 24-NOV-1992; 92WO-US010206.
XX PR 26-NOV-1991; 91US-00800458.
XX PA (ALKE-) ALKERMES INC.
XX PI Friden PM;
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XX WPI; 1993-196742/24.  
 DR N-PSDB; AAQ43848.  
 XX  
 PT Antibody conjugates specific for transferrin receptor - used for  
 PT diagnosis and treatment of cancer, AIDS and neurological disorders.  
 XX  
 XX Disclosure; Fig 19J; 151pp; English.  
 XX  
 CC The sequences given in AAR41715-18 are encoded by the expression vector  
 CC pAH4808. This vector represents the cloning of the human gamma isotype,  
 CC gamma-4, with the variable region of the murine monoclonal antibody  
 CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the  
 CC heavy chain (VH) is derived from a murine source and the sequences  
 CC encoding CH1, CH2 and CH3 are derived from a human source. This vector,  
 CC in combination with the chimeric light chain vector, pAG4611 (see also  
 CC AAQ43845), was transfected into SP2/0 cells and clones were isolated.  
 CC 128.1 is an anti-human transferrin receptor antibody which binds to the  
 CC transferrin receptor on brain capillary endothelial cells. This antibody  
 CC may be used in a conjugate in which it is linked to a neuropharmaceutical  
 CC or diagnostic agent. The conjugate may be used to treat or prevent  
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 110 AA;  
 SQ  
 Query Match 94.2%; Score 553; DB 2; Length 110;  
 Best Local Similarity 94.5%; Pred. No. 3.4e-49;  
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60  
 DB 1 APEFLGGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYDGVGVHNAKTK 60  
 QY 61 PREEQNSTYRVVSVLTVLHQLDNLGKEYCKVSNKGLPSSIEKTSKAK 110  
 DB 61 PREEQNSTYRVVSVLTVLHQLDNLGKEYCKVSNKGLPSSIEKTSKAK 110  
 RESULT 8  
 AAE28089  
 ID AAE28089 standard; protein; 109 AA.  
 AC AAE28089;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.  
 XX  
 KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;  
 KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;  
 KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;  
 KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;  
 KW virucide.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200260919-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 XX 12-DEC-2001; 2001WO-US048432.  
 PF  
 XX 12-DEC-2000; 2000US-0254884P.  
 PR  
 XX 09-MAY-2001; 2001US-0289760P.  
 XX  
 XX (MEDI-) MEDIMUNE INC.  
 PA  
 XX Dall'acqua W, Johnson LS, Ward BS;  
 PI  
 XX WPI; 2002-666925/71.  
 DR  
 XX

PT Modified immunoglobulins useful in the treatment of autoimmune diseases,  
 PT comprises at least one amino acid modification relative to a wild-type  
 PT immunoglobulin constant domain.  
 XX  
 XX Disclosure; Page 138; 147pp; English.  
 XX  
 CC The invention relates to a modified immunoglobulin (IgG1) which comprises  
 CC an Fc constant domain having at least one amino acid modification. The  
 CC immunoglobulins are used in the treatment or prevention of a disease or  
 CC disorder by passive immunotherapy for vaccinating a subject and for in  
 CC vivo diagnosis of a subject. The disease and disorders include a gamma  
 CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-  
 CC host, lymphoid malignancies and passive immunotherapies and also for the  
 CC treatment of various systemic infections. The present sequence is human  
 CC immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain  
 XX  
 XX Sequence 109 AA;  
 SQ  
 Query Match 94.0%; Score 552; DB 5; Length 109;  
 Best Local Similarity 94.5%; Pred. No. 4.3e-49;  
 Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60  
 DB 1 APELLGGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60  
 QY 61 PREEQNSTYRVVSVLTVLHQLDNLGKEYCKVSNKGLPSSIEKTSKAK 109  
 DB 61 PREEQNSTYRVVSVLTVLHQLDNLGKEYCKVSNKGLPAPIEKTSKAK 109  
 RESULT 9  
 ADH75415  
 ID ADH75415 standard; protein; 110 AA.  
 XX  
 AC ADH75415;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE CH2 region K290S variant.  
 XX  
 KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
 KW autoimmune disease.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004002587-A1.  
 XX  
 PD 01-JAN-2004.  
 XX  
 XX 20-FEB-2003; 2003US-00370749.  
 PF  
 XX 20-FEB-2002; 2002US-0358161P.  
 PR  
 XX (WATK/) WATKINS J D.  
 PA (ALLA/) ALLAN B.  
 XX  
 PI Watkins JD, Allan B;  
 XX  
 XX WPI; 2004-070755/07.  
 DR  
 XX  
 PT New composition comprising a variant of a parent polypeptide having at  
 PT least a portion of a Fc region, useful in treating e.g., autoimmune  
 PT diseases.  
 XX  
 XX Disclosure; SEQ ID NO 53; 62pp; English.  
 XX  
 CC The invention relates to a new composition comprises a variant of a  
 CC parent polypeptide having at least a portion of a Fc region. The variant  
 CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the  
 CC presence of effector cells more effectively than the parent polypeptide  
 CC and comprises at least one amino acid modification at position 280 in the  
 CC Fc region. The composition is useful in treating diseases e.g.,

CC autoimmune diseases. The present sequence represents a CH2 region  
CC variant.  
SQ Sequence 110 AA;

Query Match 94.0%; Score 552; DB 8; Length 110;  
Best Local Similarity 93.6%; Pred. No. 4.4e-49;  
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
Db 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTS 60  
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIKAK 110  
|| : |||||  
Db 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIKAK 110  
|| : |||||

RESULT 10  
ADL90103  
ID ADL90103 standard; protein; 110 AA.  
XX AC ADL90103;  
XX DT 17-JUN-2004 (first entry)  
XX DE Human immunoglobulin CH2 region, SEQ ID 2.  
XX KW Immune response; immunoglobulin; Ig; CH2 region; human.  
XX OS Homo sapiens.  
XX PN WO2004027049-A2.  
XX PD 01-APR-2004.  
XX PF 18-SEP-2003; 2003WO-US030188.  
XX PR 20-SEP-2002; 2002US-0412219P.  
XX PR 14-MAR-2003; 2003WO-US007995.  
XX PA (ASTR-) ASTRAL INC.  
XX PI Bot A, Wang L, Smith D, Phillips B;  
XX WPI; 2004-295415/27.  
XX Generating an immune response to an antigen, useful for generating  
PT desired T cell responses comprises administering an immunoglobulin having  
PT one peptide epitope of the antigen attached to the immunoglobulin.  
XX Disclosure; Page 11; 154pp; English.

The present invention relates to a method for generating an immune  
CC response to an antigen in a patient. The method comprises administering  
CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at  
CC least one peptide epitope of the antigen attached to the Ig or its  
CC portion and administering the immunoglobulin or its portion in  
CC conjunction with a RNA segment. A recombinant human Ig molecule capable  
CC of binding to an Fc gamma receptor (FcgammaR) of an antigen presenting  
CC cell (APC) was used to illustrate the invention. The recombinant human Ig  
CC molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a  
CC hinge region (ADL90104) and a flanking peptide (ADL90105).

SQ Sequence 110 AA;

Query Match 93.9%; Score 551; DB 8; Length 110;  
Best Local Similarity 93.6%; Pred. No. 5.5e-49;  
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
Db 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIKAK 110  
|| : |||||  
Db 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIKAK 110  
|| : |||||

RESULT 11  
ADH75413  
ID ADH75413 standard; protein; 110 AA.  
XX AC ADH75413;  
XX DT 22-APR-2004 (first entry)  
XX DE CH2 region D280H variant.  
XX KW Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
XX autoimmune disease.  
XX OS Unidentified.  
XX PN US2004002587-A1.  
XX PD 01-JAN-2004.  
XX PF 20-FEB-2003; 2003US-00370749.  
XX PR 20-FEB-2002; 2002US-0358161P.  
XX PA (WATK/) WATKINS J D.  
XX PA (ALLA/) ALLAN B.  
XX PI Watkins JD, Allan B;  
XX WPI; 2004-070755/07.  
XX New composition comprising a variant of a parent polypeptide having at  
PT least a portion of a Fe region, useful in treating e.g., autoimmune  
PT diseases.  
XX Disclosure; SEQ ID NO 51; 62pp; English.

The invention relates to a new composition comprises a variant of a  
CC parent polypeptide having at least a portion of a Fc region. The variant  
CC mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the  
CC presence of effector cells more effectively than the parent polypeptide  
CC and comprises at least one amino acid modification at position 280 in the  
CC Fc region. The composition is useful in treating diseases e.g.,  
CC autoimmune diseases. The present sequence represents a CH2 region  
CC variant.

SQ Sequence 110 AA;

Query Match 93.7%; Score 550; DB 8; Length 110;  
Best Local Similarity 93.6%; Pred. No. 7e-49;  
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||  
Db 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIKAK 110  
|| : |||||  
Db 61 PREEQYNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIKAK 110  
|| : |||||

RESULT 12  
AAR67438  
ID AAR67438 standard; protein; 109 AA.  
XX AC AAR67438;  
XX DT 25-MAR-2003 (revised)



DT 08-JUL-1995 (first entry)  
 XX OKT3 monoclonal antibody fragment.  
 XX  
 KW OKT3; monoclonal antibody; antibody engineering; immunosuppressive;  
 KW humanized antibody.  
 XX  
 OS Mus musculus.  
 XX  
 XX W09428027-A1.  
 PN  
 XX 08-DEC-1994.  
 PD  
 XX  
 XX 01-JUN-1994; 94WO-US006198.  
 PF  
 XX 01-JUN-1993; 93US-00070116.  
 PR  
 XX (ARCH-) ARCH DEV CORP.  
 PA  
 XX Bluestone JA, Zivin RA, Jolliffe L;  
 PI  
 XX WPI; 1995-022721/03.  
 XX P-PSDB; AAQ75356.  
 DR  
 XX New humanised OKT3 antibody with mutated Fc receptor binding region -  
 PT useful as immunosuppressant to reduce transplant rejection, lacks the T-  
 PT cell activating side effects of wild type antibody.  
 PT  
 XX Disclosure; Page 82-87; 135pp; English.  
 PS  
 XX The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-  
 CC cell activating and immunosuppressive activity, and is used to treat  
 CC transplant patients to prevent rejection. The antibody can be engineered  
 CC to contain a human Fc region. By transferring the binding specificity  
 CC into a human framework, the immunogenicity is reduced without affecting  
 CC the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 CC  
 XX Sequence 109 AA;  
 SQ  
 Query Match 93.5%; Score 549; DB 2; Length 109;  
 Best Local Similarity 94.5%; Pred. No. 8.8e-49;  
 Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 PPVAGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61  
 Db 1 PELLGGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60  
 QY 62 REEQYNSTRVRSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
 Db 61 REEQFNSTRVRSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109  
 RESULT 13  
 ADD25761  
 ID ADD25761 standard; protein; 109 AA.  
 XX  
 AC ADD25761;  
 XX  
 XX 15-JAN-2004 (first entry)  
 DT  
 XX Binding domain-immunoglobulin fusion protein-associated protein #149.  
 DE  
 XX Binding domain; immunoglobulin; fusion protein; cytostatic;  
 KW antithyroid; immunosuppressive; antidiabetic; antithyroid;  
 KW neuroprotective; hinge region; immunoglobulin heavy chain;  
 KW CH2 constant region; CH3 constant region; IgG1;  
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
 XX  
 OS Unidentified.

XX US2003118592-A1.  
 XX 26-JUN-2003.  
 XX 25-JUL-2002; 2002US-00207655.  
 XX 17-JAN-2001; 2001US-0367358P.  
 PR 17-JAN-2002; 2002US-00053530.  
 PR 03-JUN-2002; 2002US-0385691P.  
 XX (GENE-) GENE-CRAFT INC.  
 PA  
 XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
 PI WPI; 2003-801317/75.  
 XX  
 XX New binding domain-immunoglobulin fusion protein, useful for treating a  
 PT subject having or suspected of having a malignant condition or a B-cell  
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
 PT  
 XX Disclosure; SEQ ID NO 322; 157pp; English.  
 PS  
 XX The invention relates to a binding domain-immunoglobulin fusion protein  
 CC comprising a binding domain polypeptide that is fused to an  
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
 CC CH2 constant region polypeptide that is fused to the hinge region  
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
 CC polypeptide that is fused to the CH2 constant region polypeptide. The  
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
 CC immunoglobulin hinge region polypeptide contains no more than one  
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
 CC capable of at least one immunological activity comprising antibody  
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
 CC binding domain polypeptide is capable of specifically binding to an  
 CC antigen. Also included are an isolated polynucleotide encoding the  
 CC binding domain-immunoglobulin fusion protein, a recombinant expression  
 CC construct comprising the polynucleotide (operably linked to a promoter),  
 CC a host cell transformed or transfected with a recombinant expression  
 CC construct, producing the binding domain-immunoglobulin fusion protein, a  
 CC pharmaceutical composition comprising the binding domain-immunoglobulin  
 CC fusion protein or polynucleotide and a carrier, and treating a subject  
 CC having or suspected of having a malignant condition or a B-cell disorder.  
 CC The binding domain-immunoglobulin fusion protein is useful for treating a  
 CC subject having or suspected of having a malignant condition or a B-cell  
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
 CC sclerosis or autoimmune disease. The present sequence is a binding domain  
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
 CC sequence data for this patent formed part of the printed specification  
 CC and is also available in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not  
 CC identified the sequences in the printed specification by their SEQ ID  
 CC number therefore none of the sequences can be explicitly identified.  
 XX  
 SQ Sequence 109 AA;

Query Match 92.8%; Score 545; DB 7; Length 109;  
 Best Local Similarity 93.6%; Pred. No. 2.3e-48;  
 Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 PPVAGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61  
 Db 1 PELLGGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

QY	62	REEQNSTYRVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK	110
Db	61	REEQNSTYRVSVLTVLHODWLNKGKCKVSNKGLPAPIEKTISKAK	109
RESULT 14			
AAAR41709			
ID	AAAR41709	standard; protein; 109 AA.	
XX	AC	AAAR41709;	
XX	DT	25-MAR-2003 (revised)	
XX	DT	20-OCT-1993 (first entry)	
XX	DE	Undefined ORF2 encoded by plasmid pAH4625.	
XX	KW	Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;	
XX	KW	light; chain; variable; constant; region; anti-human; pAH4807;	
XX	KW	transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;	
XX	KW	endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;	
XX	KW	diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;	
XX	KW	Parkinsons disease; Alzheimers disease; SP2/0 cell.	
XX	OS	Synthetic.	
XX	PN	WO9310819-A1.	
XX	PD	10-JUN-1993.	
XX	PF	24-NOV-1992; 92WO-US010206.	
XX	PR	26-NOV-1991; 91US-00800458.	
XX	PA	(ALKE-) ALKERMES INC.	
XX	PI	Friden PM;	
XX	DR	WPI; 1993-196742/24.	
XX	DR	N-PSDB; AAQ43846.	
XX	PT	Antibody conjugates specific for transferrin receptor - used for	
XX	PT	diagnosis and treatment of cancer, AIDS and neurological disorders.	
XX	PS	Disclosure; Fig 17J; 151pp; English.	
XX	CC	The sequences given in AAR41707-09 are encoded by the expression vector	
XX	CC	pAH4625. This vector represents the cloning of the human gamma isotype,	
XX	CC	gamma-2, with the variable region of the murine monoclonal antibody	
XX	CC	128.1. This plasmid encodes a chimeric monoclonal antibody in which the	
XX	CC	heavy chain (VH) is derived from a murine source and the sequences	
XX	CC	encoding CH1, CH2 and CH3 are derived from a human source. This vector,	
XX	CC	in combination with the chimeric light chain vector, pAG4611 (see also	
XX	CC	AAQ43845), was transfected into SP2/0 cells and clones were isolated.	
XX	CC	128.1 is an anti-human transferrin receptor antibody which binds to the	
XX	CC	transferrin receptor on brain capillary endothelial cells. This antibody	
XX	CC	may be used in a conjugate in which it is linked to a neuropharmaceutical	
XX	CC	or diagnostic agent. The conjugate may be used to treat or prevent	
XX	CC	neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,	
XX	CC	Parkinsons and Alzheimers disease. It may also be used for diagnostic	
XX	CC	methods. (Updated on 25-MAR-2003 to correct PN field.)	
XX	SQ	Sequence 109 AA;	
Query Match 92.6%; Score 543.5; DB 2; Length 109;			
Best Local Similarity 92.7%; Pred. No. 3.3e-48;			
Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;			
QY	1	APPVAGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATK	60
Db	1	APPVA-GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATK	59
QY	61	REEQNSTYRVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK	110

Db	60	REEQNSTYRVSVLTVLHODWLNKGKCKVSNKGLPAPIEKTISKTK	109
RESULT 15			
AAAY54997			
ID	AAAY54997	standard; protein; 109 AA.	
XX	AC	AAAY54997;	
XX	DT	17-FEB-2000 (first entry)	
XX	DE	Mutated CH2 sequence G2deltaa.	
XX	KW	Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;	
XX	KW	cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;	
XX	KW	B cell activation; mast cell degranulation; phagocytosis; vasculitis;	
XX	KW	Crohn's disease; graft-vs-host disease; organ transplant rejection;	
XX	KW	bone-marrow transplant rejection; autoimmune disease; asthma; allergy;	
XX	KW	allergic disorder; autoimmune haemolytic anaemia; inflammatory disease;	
XX	KW	autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;	
XX	KW	neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;	
XX	KW	sickle cell anaemia; coronary artery occlusion.	
XX	OS	Synthetic.	
XX	PN	WO9958572-A1.	
XX	PD	18-NOV-1999.	
XX	PF	07-MAY-1999; 99WO-GB001441.	
XX	PR	08-MAY-1998; 98GB-00009951.	
XX	PA	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.	
XX	PI	Armour KL, Clark MR, Williamson LM;	
XX	DR	WPI; 2000-039075/03.	
XX	PT	Immunoglobulin-derived binding molecules that do not activate complement	
XX	PT	or trigger cytotoxic activities and maintaining desirable immunoglobulin	
XX	PS	properties.	
XX	PS	Claim 12; Fig 17; 81pp; English.	
XX	CC	This sequence represents the mutated CH2 molecule G2deltaa, and is a	
XX	CC	binding molecule of the invention. The recombinant binding molecule is	
XX	CC	capable of binding a target molecule without triggering complement	
XX	CC	dependent lysis, or the cell-mediated destruction of the target	
XX	CC	comprises: (a) a binding domain capable of binding a target molecule; and	
XX	CC	(b) an effector domain that is homologous to all or part of a constant	
XX	CC	domain of a human immunoglobulin G (IgG) heavy chain. The binding	
XX	CC	molecule is used to bind a target molecule (especially FcgammaRIIb	
XX	CC	causing inhibition of B cell activation, mast cell degranulation or	
XX	CC	phagocytosis). The binding molecule can be used to prevent or inhibit the	
XX	CC	binding of a second binding molecule, e.g. an antibody, to the target	
XX	CC	molecule. The binding molecule is useful for the treatment of graft-vs-	
XX	CC	host disease, organ transplant rejection, bone-marrow transplant	
XX	CC	rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,	
XX	CC	autoimmune thrombocytopenia and arthritis), autoimmunity (e.g.	
XX	CC	foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),	
XX	CC	chronic or acute inflammatory diseases (e.g. Crohn's, HDN	
XX	CC	(erythroblastosis foetalis), Goodpastures, sickle cell anaemia and	
XX	CC	coronary artery occlusion). The binding molecules do not activate	
XX	CC	complement or trigger cytotoxic activities through FcgammaR and desirable	
XX	CC	IgG properties have been retained. The polypeptides do not contain non-	
XX	CC	human amino acids, and are therefore likely to have reduced	
XX	CC	immunogenicity. Further, they still bind Protein A, which is consistent	
XX	CC	with being able to cross the human placenta through interaction with FcRn	
XX	CC	(neonatal Fc receptor)	
XX	SQ	Sequence 109 AA;	

Query Match 92.6%; Score 543.5; DB 3; Length 109;  
Best Local Similarity 93.6%; Pred. No. 3.3e-48;  
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;  
QY 1 APPVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKNNYVDGVEVHNAKTK 60  
Db 1 APPVA-GPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKNNYVDGVEVHNAKTK 59  
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
Db 60 PREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIISKTK 109

Search completed: November 17, 2005, 07:47:00  
Job time : 89.9087 secs

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Query Match 24.0%; Score 141; DB 2; Length 107;  
 Best Local Similarity 31.4%; Pred. No. 6.2e-07;  
 Matches 32; Conservative 21; Mismatches 47; Indels 2; Gaps 2;  
 QY 7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66  
 DB 6 GVITVLIPLSPDL-LYONGAPKLTCLVVDLESE-KNVNVTWQEKKTPVSAQSWYTKHHH 63  
 QY 67 NSTYRVSVLTVLHQDLNKGKKYCKVSNKGLPSSIEKTIISK 108  
 DB 64 NATTSITSLPVVAKDWIEGYQCIVDHPDFPKPIVRSITK 105  
 RESULT 3  
 I68730  
 IGE chain C3 region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
 C:Accession: I68730  
 R:Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.  
 Immunogenetics 27, 288-292, 1988  
 A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s  
 A:Reference number: I5443; MUID:88152907; PMID:3346043  
 A:Accession: I68730  
 A>Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <RES>  
 A:Cross-references: GB:I2933; NID:9194464; PIDN:AAA37915.1; PID:9194469  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:22-90/domain: immunoglobulin homology <IMM>  
 Query Match 23.5%; Score 138; DB 2; Length 107;  
 Best Local Similarity 30.7%; Pred. No. 1.2e-06;  
 Matches 35; Conservative 21; Mismatches 32; Indels 26; Gaps 5;  
 QY 7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDV-SHEDPEVKFN-----WYVDGVEV 54  
 DB 6 GVITVLIPLSPDL-LYONGAPKLTCLVVDLESEKVNVTWQEKTSVSASQWY---TKH 61  
 QY 55 HNAKTKPREQNSTYRVSVLTVLHQDLNKGKKYCKVSNKGLPSSIEKTIISK 108  
 DB 62 HN-----NATTSITSLPVVAKDWIEGYQCIVDHPDFPKPIVRSITK 105  
 RESULT 4  
 K3HU  
 Ig kappa chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1980 #sequence\_revision 02-Jul-1998 #text\_change 09-Jul-2004  
 C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02  
 R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.  
 Biochemistry 9, 3155-3161, 1970  
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc  
 A:Reference number: A90562; MUID:71064023; PMID:5489770  
 A:Contents: myeloma protein Eu  
 A:Accession: B90562  
 A:Molecule type: protein  
 A:Residues: 1-106 <GOT>  
 A:Cross-references: UNIPROT:P01834  
 A>Note: This sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
 R:Gall, W.E.; Edelman, G.M.  
 Biochemistry 9, 3188-3196, 1970  
 A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
 A:Reference number: A90565; MUID:71064027; PMID:4923144  
 A:Contents: annotation; Eu, disulfide bonds  
 R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
 A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub  
 A:Reference number: A91651; MUID:72188439; PMID:5027703  
 A:Contents: Bence Jones protein T1  
 A:Accession: A91651  
 A:Molecule type: protein

A:Residues: 1-106 <SUT>  
 R:Hieter, P.A.; Max, B.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.  
 Cell 22, 197-207, 1980  
 A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conser  
 A:Reference number: A90806; MUID:81042304; PMID:6775818  
 A:Accession: A90806  
 A:Molecule type: DNA  
 A:Residues: 1-106 <HIB>  
 A:Cross-references: GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148  
 A>Note: the sequence was determined from the germline gene  
 R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,  
 in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,  
 A:Reference number: A94417  
 A:Contents: Bence Jones protein Roy  
 A:Accession: A94417  
 A:Molecule type: protein  
 A:Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>  
 A>Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu  
 R:Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
 A:Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).  
 A:Reference number: A91639; MUID:68242259; PMID:5586923  
 A:Contents: Bence Jones protein Cum  
 A:Accession: A91639  
 A:Molecule type: protein  
 A:Residues: 1-56, 'Q', 58-106 <HI2>  
 R:Titani, K.; Shinoda, T.; Putnam, F.W.  
 J. Biol. Chem. 244, 3550-3560, 1969  
 A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete  
 A:Reference number: A92047; MUID:69234734; PMID:4893682  
 A:Contents: Bence Jones protein Ag  
 A:Accession: A92047  
 A:Molecule type: protein  
 A:Residues: 1-13, 'N', 15-106 <TIT>  
 R:Kohler, H.; Shimizu, A.; Faul, C.; Putnam, F.W.  
 Science 169, 56-59, 1970  
 A:Title: Macroglobulin structure: variable sequence of light and heavy chains.  
 A:Reference number: A94242; MUID:70201507; PMID:5447531  
 A:Contents: Waldenstrom's macroglobulin Ou  
 A:Accession: A94242  
 A:Molecule type: protein  
 A:Residues: 1-13, 'N', 15-106 <KOH>  
 R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
 Am. J. Hum. Genet. 48, 613-620, 1991  
 A:Title: Km typing with PCR: application to population screening.  
 A:Reference number: A37927; MUID:91150772; PMID:1900145  
 A:Accession: B37927  
 A>Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 8-106 <KUR>  
 A>Note: allotype Inv(3)  
 R:Steiner, V.; Chang, J.Y.  
 FEBS Lett. 222, 6-10, 1987  
 A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
 A:Reference number: S02572; MUID:88005152; PMID:3115831  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: GDB:IGKC  
 A:Cross-references: GDB:120088; OMIM:147200  
 A:Map position: 2p12-2p12  
 C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kai  
 hain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into l  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-88/Domain: immunoglobulin homology <IMM>  
 F:126-86/Disulfide bonds: #status experimental  
 F:106/Disulfide bonds: interchain (to heavy chain) #status experimental  
 Query Match 22.3%; Score 131; DB 1; Length 106;  
 Best Local Similarity 30.5%; Pred. No. 6e-06;  
 Matches 32; Conservative 24; Mismatches 43; Indels 6; Gaps 3;  
 QY 8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPREQ 65







RESULT 13

F53275  
Ig kappa-1 chain C region b95 allotype - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
A:Accession: F53275  
R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.  
Immunogenetics 34, 201-207, 1991  
A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.  
A:Reference number: A53275; MUID:91372868; PMID:1909995  
A:Accession: F53275  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-104 <AYA>  
A>Note: sequence inconsistent with nucleotide translation  
A>Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:56170)  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-87/Domain: immunoglobulin homology <IMM>

Query Match 19.8%; Score 116; DB 2; Length 104;  
Best Local Similarity 29.1%; Pred. No. 0.00018;  
Matches 32; Conservative 25; Mismatches 39; Indels 14; Gaps 6;  
QY 3 PVAGPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE-----VHNAK 58  
DB 2 PVA--PTVLIFPPSPAE--LATGTATIVCV--ANKYFPDVTVTWKVDGTTQTGTIENS 54  
QY 59 TKPREQVNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSK 108  
DB 55 TQNSD--DCTNLSSTLTLSKDEYNSHDEYICQVA-QSGSPVQVQFSR 101

RESULT 14

A37927  
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
A:Accession: A37927  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: A37927  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 19.6%; Score 115; DB 2; Length 99;  
Best Local Similarity 28.4%; Pred. No. 0.00021;  
Matches 29; Conservative 24; Mismatches 43; Indels 6; Gaps 3;  
QY 11 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPREQVNS 68  
DB 1 FIFP--PSDEQLKSGTASVCLLNFPYR--EAKVQWKVDNALQSGNSQESVTEQDSKDS 56  
QY 69 TYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 110  
DB 57 TYSLSSTLTLSKADYKHKLYACEVTHOGLSPVTKSFNRGE 98

RESULT 15

B34509  
Ig light chain C region 3 - sandbar shark (fragment)  
C:Species: Carcharhinus plumbeus (sandbar shark)  
C:Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 17-Nov-2000  
A:Accession: B34509  
R:Schluter, S.F.; Hohman, V.S.; Edmondson, A.B.; Marchalonis, J.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989  
A:Title: Evolution of immunoglobulin light chains: cDNA clones specifying sandbar shark

A:Reference number: A34509; MUID:90099382; PMID:2513577  
A:Accession: B34509  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <SCH>  
A:Cross-references: GB:M29044; NID:g212941; PIDN:AAA49153.1; PID:g212942  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
Query Match 19.4%; Score 114; DB 2; Length 102;  
Best Local Similarity 31.5%; Pred. No. 0.00027;  
Matches 29; Conservative 18; Mismatches 41; Indels 4; Gaps 3;  
QY 8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG--VEVINAATKPREEQY 66  
DB 13 PSVSLLPSP--DQITAKNTATLVLVSGFKPGAABIE--WTVDGSGVRGNGVETSRVQOEA 69  
QY 67 NSTYRVSVLTVLHODWLNKGKEYCKVSNKGL 98  
DB 70 DNTFVSSTLTLSASDWNWSHLYSCLVKREAL 101  
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Job time : 16.5753 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.8539 Seconds  
(without alignments)  
723.518 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVFLFPKPKD.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	22.3	106	1 KAC_HUMAN	P01834 homo sapien
2	130	22.1	103	1 LAC_CHICK	P20763 gallus gall
3	121.5	20.7	105	1 LAC1_MOUSE	P01843 mus musculus
4	121.5	20.7	105	1 LAC5_MOUSE	P20765 mus musculus
5	117.5	20.0	105	1 LAC5_MOUSE	P20764 mus musculus
6	112.5	19.2	106	2 Q8TCJ5	P01845 mus musculus
7	112	19.1	103	1 KAC4_RABIT	P01840 oryctolagus
8	109.5	18.7	105	1 LAC_HUMAN	P01842 homo sapien
9	108.5	18.5	105	1 LAC_RABIT	P01847 oryctolagus
10	104	17.7	104	1 KAC6_RABIT	P03984 oryctolagus
11	103	17.5	106	1 KAC_MOUSE	P01837 mus musculus
12	101	17.2	104	1 LAC1_RAT	P20766 rattus norv
13	99.5	17.0	105	1 LAC_PIG	P01846 sus scrofa
14	98.5	16.8	106	1 KACB_RABIT	P01839 oryctolagus
15	95	16.2	104	1 LAC2_RAT	P20767 rattus norv
16	95	16.2	106	1 KACB_RAT	P01835 rattus norv
17	92.5	15.8	104	1 KAC9_RABIT	P01838 oryctolagus
18	92	15.7	103	1 KAC5_RABIT	P01841 oryctolagus
19	90	15.3	104	1 LAC3_MOUSE	P01845 mus musculus
20	90	15.3	106	1 KAC_RAT	P01836 rattus norv
21	76	12.9	104	1 LAC2_MOUSE	P01844 mus musculus
22	76	12.9	105	2 Q9JG1	P01844 mus musculus
23	66	11.2	107	2 Q8EY10	P01844 mus musculus
24	66	11.2	107	2 Q8EY10	P01844 mus musculus
25	63	10.7	98	2 Q7XZF9	P01844 mus musculus
26	62	10.6	93	2 Q6LBN9	P01844 mus musculus
27	61.5	10.5	93	2 Q6LBN9	P01844 mus musculus
28	61	10.4	91	2 Q9JG1	P01844 mus musculus
29	60.5	10.3	74	2 P79659	P01844 mus musculus
30	60.5	10.3	74	2 P79660	P01844 mus musculus
31	60	10.2	73	2 Q8FBY4	P01844 mus musculus

32	59	10.1	79	1 SNRP_HUMAN	P80697 homo sapien
33	59	10.1	91	2 Q31248	Q31248 peromyscus
34	59	10.1	93	2 Q31158	Q31158 mus musculus
35	58.5	10.0	55	2 Q768W8	Q768W8 mus musculus
36	58.5	10.0	93	2 O19471	O19471 mus musculus
37	58.5	10.0	93	2 O19472	O19472 mus musculus
38	58.5	10.0	93	2 Q9QUH8	Q9QUH8 mus musculus
39	58	9.9	103	2 Q8HX76	Q8HX76 sus scrofa
40	58	9.9	104	2 Q8C5T6	Q8C5T6 mus musculus
41	58	9.9	106	2 Q31261	Q31261 rattus norv
42	57.5	9.8	55	2 Q768W5	Q768W5 mus musculus
43	57.5	9.8	65	1 DN71_SULAC	P13123 sulfolobus
44	57.5	9.8	95	1 DAFI_TRYCR	Q26327 trypanosoma
45	57	9.7	90	1 ALB2_SULTO	Q97166 sulfolobus

#### ALIGNMENTS

#### RESULT 1

ID	KAC_HUMAN	STANDARD	PRT	106 AA
AC	P01834			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	IG kappa chain C region.			
GN	Name=IGKC;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hesse M., Langer B., Ponstingl H.,			
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			



```
Query Match      22.1%; Score 130; DB 1; Length 103;
Best Local Similarity 31.2%; Pred. NO. 3.5e-05;
Matches 34; Conservative 25; Mismatches 42; Indels 8; Gaps 6;

QY 2 PPVAGGSPFLPPKPKDLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKP 61
DB 2 PKVA--PTTLTPPPS--KEELNEATKATLVCLINDF--YPSP-VTVDWIIDG--STRSGETTA 55

QY 62 RBEQNSTYRVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 56 PQRSNSQYMASSYLSASDSSSHETTCRVTHNG--TSIYKTKRSE 102

RESULT 3
LAC1 MOUSE
ID LAC1 MOUSE STANDARD; PRT; 105 AA.
AC P01843;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83014953; PubMed=6812053;
RA Selsing E., Miller J., Wilson R., Storb U.;
RT "Evolution of mouse immunoglobulin lambda genes.";
RT Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE=81148806; PubMed=6259534;
RA Botwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA Geffer M.L., Baltimore D.;
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RT Nature 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE=82220143; PubMed=6283385;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RT Nature 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=71107854; PubMed=5276767;
RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
CC -!- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
CC normal lambda-2 chain and 1 abnormal lambda-1 chain that is
CC missing a large part of the V region. The C region sequence (shown
CC here) appears completely normal.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00582; AAA51636.1; -
CC DR EMBL; J00587; AAB59672.1; -
CC PIR; A93922; L1MS.
CC PDB; 1JNH; X-ray; A=1-105.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
```

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DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS0290; IG_MHC; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 100 Ig-like.
FT DOMAIN 6 100
FT DISULFID 27 86
FT DISULFID 104 104
FT CONFLICT 19 20 Interchain (with heavy chain).
FT CONFLICT 56 56 ET -> TE (in Ref. 4).
FT CONFLICT 75 75 Q -> E (in Ref. 4).
FT CONFLICT 81 82 Missing (in Ref. 4).
FT CONFLICT 85 85 HS -> SH (in Ref. 4).
FT CONFLICT 96 96 S -> SS (in Ref. 4).
FT STRAND 4 4 E -> Q (in Ref. 4).
FT STRAND 7 7
FT STRAND 10 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 22 33
FT STRAND 37 43
FT TURN 44 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 52 54
FT STRAND 58 60
FT TURN 61 63
FT STRAND 64 74
FT HELIX 75 80
FT STRAND 84 90
FT TURN 91 92
FT STRAND 93 99
SQ SEQUENCE 105 AA; A89F2B09BCFCA018 CRC64;

Query Match      20.7%; Score 121.5; DB 1; Length 105;
Best Local Similarity 31.1%; Pred. NO. 0.00025;
Matches 32; Conservative 18; Mismatches 46; Indels 7; Gaps 3;

QY 8 PSVLFPPKPKDLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREQY 66
DB 6 PSVTLFPPSSEEL----ETNKATLVCTITDFYGVVTVDMKVDGTPVTQGMETTPQSKS 61

QY 67 NSTYRVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 109
DB 62 NKKYMASSYLTLTARAWERHSSYSCQVTHEG--HTVEKSLSR 102

RESULT 4
LAC5 MUSSP
ID LAC5 MUSSP STANDARD; PRT; 105 AA.
AC P20765;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-5 chain C region.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88196070; PubMed=3129289;
RA Mami F., Cazenave P.A., Kindt T.J.;
RT "Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
RL EMBO J. 7:117-122(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; V00807; CAA24189.1; -
CC PIR; B90262; KIMS.
CC DR PDB; 1AIF; X-ray; A/L=1-106.
CC DR PDB; 1FSK; X-ray; B/E=1-106.
CC DR PDB; 1KB5; X-ray; L=1-106.
CC DR PDB; 1KCR; X-ray; L=1-106.
CC DR PDB; 1KCS; X-ray; L=1-106.
CC DR PDB; 1KCU; X-ray; L=1-106.
CC DR PDB; 1KCV; X-ray; L=1-106.
CC DR PDB; 1LOR; X-ray; A=1-106.
CC DR PDB; 1ORS; X-ray; A=1-106.
CC DR PDB; 25C8; X-ray; L=1-103.
CC DR MGD; MGI:96495; Igc-C.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003597; Ig cl.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00407; Igc1; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1 102
FT DOMAIN 5 102
FT DISULFID 26 86
FT DISULFID 106 106
FT STRAND 3 3
FT STRAND 6 10
FT HELIX 14 17
FT TURN 18 20
FT STRAND 21 32
FT STRAND 37 42
FT TURN 43 44
FT STRAND 45 47
FT TURN 49 50
FT STRAND 51 55
FT TURN 60 62
FT STRAND 65 74
FT HELIX 75 79
FT TURN 80 80
FT STRAND 83 89
FT TURN 91 92
FT STRAND 97 102
FT TURN 103 106
SQ SEQUENCE 106 AA; 11778 MW; 4B51FF5EF49BAEB5 CRC64;

Query Match 17.5%; Score 103; DB 1; Length 106;
Best Local Similarity 27.2%; Pred. No. 0.017;
Matches 28; Conservative 22; Mismatches 47; Indels 6; Gaps 3;

Qy 8 PSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA--KTKPREEQ 65
Db 5 PTVSIFPPSSSQ--LTSGASVVCFLANNFYPKDINVK--WKIDGSRQNGVLSWTDQDS 60
Qy 66 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIK 108
Db 61 KDTYSMSSTLTATKDEVERHNSYTCATHTKTSPIVKSPNR 103

RESULT 12
LAC1_RAT
ID LAC1_RAT
AC P20766;
STANDARD; PRT; 104 AA.

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DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
RL Gene 55:75-84(1987).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.ieb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M22520; AAA41419.1; ALT_INIT.
CC HSP; P01843; LTNH.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00407; Igc1; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1 99
FT DOMAIN 6 99
FT DISULFID 27 85
FT DISULFID 103 103
SQ SEQUENCE 104 AA; 11565 MW; CBF71811F4BC878A CRC64;

Query Match 17.2%; Score 101; DB 1; Length 104;
Best Local Similarity 24.3%; Pred. No. 0.027;
Matches 25; Conservative 23; Mismatches 49; Indels 6; Gaps 2;

Qy 8 PSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKRREQYN 67
Db 6 PSVTLFPSPSEEL---KTDKATLVCMVTDYFGVMTVVMKADGTPITQGVETTPQPKQN 61
Qy 68 STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 62 NKYWTATSYLLLTAKAWETHSNYSQVTHE--ENTVEKLSRAE 102

RESULT 13
LAC_PIG
ID LAC_PIG
AC P01846; STANDARD; PRT; 105 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=78000254; PubMed=409425;
RA Novotny J., Franek P., Margolies M.N., Haber E.;
RT "Amino acid sequence of normal (microheterogeneous) porcine
RL immunoglobulin lambda chains."
RL Biochemistry 16:3765-3772(1977).

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CC -!- MISCELLANEOUS: This chain was obtained from a mixture of normal
CC immunoglobulins.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02129; L1PG.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 2 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
SQ SEQUENCE 105 AA; 11003 MW; 3817AAEBD747C396 CRC64;

Query Match 17.0%; Score 99.5; DB 1; Length 105;
Best Local Similarity 27.6%; Pred. No. 0.039;
Matches 29; Conservative 20; Mismatches 47; Indels 9; Gaps 4;

QY 8 PSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA--KTKPRSEQ 65
DB 6 PTVNLFPSSSEL-----GTNKAATVCLISDFYPGAVTVTKAGGTTVVGVEVTKRP-SKQ 60

QY 66 VNSTYRVVSVLTVLHODWLNGKEYKCKVSKNKGKLPSSIEKTSKAK 110
DB 61 SNKKAASLYALSADKSSSGFTCVTHEG--TIVEKTVTPSE 103

RESULT 14
KACB_RABIT STANDARD; PRT; 106 AA.
AC P01839;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IG kappa-b4 chain C region.
GN Name=K-BAS;
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11894960;
RX STRAIN=Basilea;
RA Heidmann O., Rougeon F.;
RT "Multiplicity of constant kappa light chain genes in the rabbit genome: a b4b4 homozygous rabbit contains a kappa-bas gene.";
RL EMBO J. 2:437-441(1983).
CC -!- MISCELLANEOUS: In Basilea rabbits, the major type of light chain is lambda. The kappa chain shown is a minor component. All other rabbit B allotypes have Cys-64.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----
CC EMBL; V01241; CAA24558.1; -;
CC PIR; A02121; K4RBS.
CC HSSP; P01837; 25C8.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
```

```
DR Pfam; PF00047; ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 87
FT DISULFID 106 106 Interchain (with a heavy chain).
SQ SEQUENCE 106 AA; 11279 MW; AF9B928DDA853849 CRC64;

Query Match 16.8%; Score 98.5; DB 1; Length 106;
Best Local Similarity 29.1%; Pred. No. 0.049;
Matches 32; Conservative 21; Mismatches 44; Indels 13; Gaps 6;

QY 3 PVAGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE----VHNAK 58
DB 3 PVA--PSVLLFPSSKEE--LTGTATIVCVANKFYPSD--ITVTWKVDGTTQQSGIENSK 56

QY 59 TKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSKNKGKLPSSIEKTSK 108
DB 57 TPQSPF--DNTYSLSSTLSLTSQAQNSHVSVTCEVV--QGSASPIVQSFNR 103

RESULT 15
LAC2_RAT STANDARD; PRT; 104 AA.
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-2 chain C region.
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----
CC EMBL; M22521; AAA41420.1; ALT_INIT.
CC HSSP; P01842; 2MCG.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00407; Igc1; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85
FT DISULFID 103 103 Interchain (with heavy chain).
SQ SEQUENCE 104 AA; 11318 MW; F087906DE43F7276 CRC64;

Query Match 16.2%; Score 95; DB 1; Length 104;
Best Local Similarity 21.4%; Pred. No. 0.11;
Matches 22; Conservative 27; Mismatches 48; Indels 6; Gaps 3;

QY 8 PSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYN 67
```



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# OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.6073 Seconds  
(without alignments)  
347.833 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APVAGGPSVFLPPPKPDT.....CKVSNKGLPSSEKTIISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/PCUTUS\_COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	94.9	110	3	US-08-444-644-21
2	557	94.9	110	3	US-08-232-246A-21
3	553	94.2	110	3	US-08-444-644-44
4	553	94.2	110	3	US-08-232-246A-44
5	549	93.5	109	2	US-08-070-116A-4
6	549	93.5	109	3	US-08-557-050-4
7	543.5	92.6	109	3	US-08-444-644-30
8	543.5	92.6	109	3	US-08-232-246A-30
9	541	92.2	105	2	US-08-232-539D-60
10	533	90.8	110	3	US-08-444-644-38
11	533	90.8	110	3	US-08-232-246A-38
12	344	58.6	66	3	US-08-569-147-85
13	175	29.8	107	4	US-09-281-760B-36
14	166.5	28.4	106	2	US-08-232-539D-54
15	152	25.9	109	3	US-08-466-163B-1
16	152	25.9	109	4	US-09-802-096-1
17	152	25.9	109	4	US-09-802-077-1
18	141	24.0	100	1	US-08-422-091-10
19	141	24.0	100	1	US-08-422-091-10
20	141	24.0	100	2	US-08-422-092-10
21	141	24.0	100	2	US-08-788-800-7
22	141	24.0	100	3	US-08-422-093-10
23	141	24.0	100	3	US-08-422-112-10
24	131.5	22.4	109	2	US-08-646-981-6
25	131	22.3	105	3	US-09-025-769B-166
26	131	22.3	105	4	US-09-490-070A-166
27	131	22.3	105	4	US-09-490-153-166

28 131 22.3 105 4 US-09-490-324-166 Sequence 166, Appl  
29 131 22.3 106 2 US-08-378-939-40 Sequence 40, Appl  
30 131 22.3 106 2 US-08-761-277A-49 Sequence 49, Appl  
31 131 22.3 106 3 US-08-444-644-26 Sequence 26, Appl  
32 131 22.3 106 3 US-08-232-246A-26 Sequence 26, Appl  
33 131 22.3 107 1 US-08-422-101-8 Sequence 8, Appl  
34 131 22.3 107 1 US-08-422-091-8 Sequence 8, Appl  
35 131 22.3 107 2 US-08-422-092-8 Sequence 8, Appl  
36 131 22.3 107 2 US-08-788-800-5 Sequence 5, Appl  
37 131 22.3 107 3 US-08-422-093-8 Sequence 5, Appl  
38 131 22.3 107 3 US-08-422-112-8 Sequence 8, Appl  
39 131 22.3 107 3 US-09-301-593-20 Sequence 20, Appl  
40 131 22.3 108 4 US-09-313-942-13 Sequence 13, Appl  
41 129 22.0 106 1 US-08-399-106A-7 Sequence 7, Appl  
42 129 22.0 106 1 US-08-433-105A-7 Sequence 7, Appl  
43 129 22.0 106 2 US-08-434-869A-7 Sequence 8, Appl  
44 128 21.8 109 1 US-08-436-463-8 Sequence 8, Appl  
45 128 21.8 109 1 US-08-024-253-8 Sequence 8, Appl

## ALIGNMENTS

RESULT 1

US-08-444-644-21  
; Sequence 21, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-21

Query Match          94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 2
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21

Query Match          94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-44

Query Match          94.2%; Score 553; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 6.2e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
```

RESULT 4  
US-08-232-246A-44  
; Sequence 44, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,246A  
; FILING DATE: 04-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-232-246A-44

Query Match 94.2%; Score 553; DB 3; Length 110;  
Best Local Similarity 94.5%; Pred. No. 6.2e-58;  
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
Db 1 APEFLGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
QY 61 PREEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
Db 61 PREEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 5  
US-08-070-116A-4  
; Sequence 4, Application US/08070116A  
; Patent No. 5885573  
; GENERAL INFORMATION:  
; APPLICANT: Zivin, Robert A.  
; APPLICANT: Jolliffe, Linda K.

; APPLICANT: Bluestone, Jeffrey A.  
; TITLE OF INVENTION: Methods and Materials For Modulation  
; TITLE OF INVENTION: of the Immuno-suppressive Activity and  
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/070,116A  
; FILING DATE: 01-JUN-1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:082  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-070-116A-4

Query Match 93.5%; Score 549; DB 2; Length 109;  
Best Local Similarity 94.5%; Pred. No. 1.8e-57;  
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 PPVAGGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 61  
Db 1 PEFGLGSPVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
QY 62 REEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
Db 61 REEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 6  
US-08-557-050-4  
; Sequence 4, Application US/08557050  
; Patent No. 6491916  
; GENERAL INFORMATION:  
; APPLICANT: Bluestone, Jeffrey A.  
; APPLICANT: Zivin, Robert A.  
; APPLICANT: Jolliffe, Linda K.  
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF  
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: protein
; US-08-557-050-4

Query Match          93.5%; Score 549; DB 4; Length 109;
Best Local Similarity 94.5%; Pred. No. 1.8e-57;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 PPVAGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 1 PEFGLGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

QY 62 REEQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 61 REEQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKGLPSSIEKTIISKAK 109

RESULT 7
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match          92.6%; Score 543.5; DB 3; Length 109;
Best Local Similarity 92.7%; Pred. No. 8.3e-57;
Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 APPVAGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59

QY 61 PREEQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 60 PREEQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKGLPAPIEKTIISKAK 109

RESULT 8
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240

```





```
RESULT 11
US-08-232-246A-38
; Sequence 38, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-38

Query Match 90.8%; Score 533; DB 3; Length 110;
Best Local Similarity 90.9%; Pred. No. 1.5e-55;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
;
Db 1 APELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
;
QY 61 PREEQNSTYRVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIISKAK 110
;
Db 61 LREEQNSTFRVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTIISKAK 110
;

RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
```

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; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-85

Query Match 58.6%; Score 344; DB 3; Length 66;
Best Local Similarity 95.5%; Pred. No. 2e-33;
Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
;
Db 1 APELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
;
QY 61 PREEQ 66
;
Db 61 PREEQ 66
;

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (413)..(414)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (451)..(451)  
OTHER INFORMATION: "n" stands for any nucleic acid  
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NAME/KEY: misc feature  
LOCATION: (460)..(462)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (500)..(500)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (530)..(530)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (568)..(568)  
OTHER INFORMATION: "n" stands for any nucleic acid  
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NAME/KEY: misc feature  
LOCATION: (847)..(849)  
OTHER INFORMATION: "n" stands for any nucleic acid  
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NAME/KEY: misc feature  
LOCATION: (853)..(853)  
OTHER INFORMATION: "n" stands for any nucleic acid  
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NAME/KEY: misc feature  
LOCATION: (1382)..(1382)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1832)..(1832)  
OTHER INFORMATION: "n" stands for any nucleic acid  
US-09-281-760E-36

Query Match 29.8%; Score 175; DB 4; Length 107;  
Best Local Similarity 35.0%; Pred. No. 4.3e-13;  
Matches 36; Conservative 23; Mismatches 42; Indels 2; Gaps 2;  
QY 7 GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66  
Db 5 GVSSYLSPPSPDL-LVYHKAPKITCLVLDLATWE-GMNLTYRESKEPVNPPVPLNKKDHF 62  
QY 67 NSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKA 109  
Db 63 NGTITVTSTLPVNTDWDIEGETYCKRVTHPHLPKDIVRSIAKA 105

RESULT 14  
US-08-232-539D-54  
Sequence 54, Application US/08232539D  
Patent No. 5965709  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: IGE Antagonists  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/178583  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-54  
Query Match 28.4%; Score 166.5; DB 2; Length 106;  
Best Local Similarity 34.3%; Pred. No. 4.4e-12;  
Matches 35; Conservative 22; Mismatches 44; Indels 1; Gaps 1;  
QY 7 GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66  
Db 1 GVSAYLSRPPSPFD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEEQY 59  
QY 67 NSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIK 108  
Db 60 NGTLTSTLPVGTDRDIEGETYQCRVTHPHLPALMRSTTK 101

RESULT 15  
US-08-466-163B-1  
Sequence 1, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 1  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-466-163B-1

Query Match 25.9%; Score 152; DB 3; Length 109;  
Best Local Similarity 34.3%; Pred. No. 2.4e-10;  
Matches 35; Conservative 21; Mismatches 44; Indels 2; Gaps 2;  
QY 7 GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66  
Db 6 GVSAYLSRPPSPFD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEEQY 64  
QY 67 NSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIK 108

Db 65 NGTLTVTSLPVGTRDWIEG-ETQCRVTHPHLPALMRSTTK 105

Search completed: November 17, 2005, 07:53:56  
Job time : 24.6073 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:47:15 ; Search time 83.1279 Seconds  
(without alignments)  
553.666 Million cell updates/sec

Title: US-09-674-857-3  
Perfect score: 587  
Sequence: 1 APPVAGGSPVFLPPPKPKOT.....CKVSNKGLPSSTKTSKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 892101

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	579	98.6	110	18	US-10-959-318-9
2	579	98.6	110	18	US-10-959-318-10
3	565	96.3	110	18	US-10-959-318-13
4	565	96.3	110	18	US-10-959-318-14
5	563	95.9	110	18	US-10-959-318-7
6	563	95.9	110	18	US-10-959-318-8
7	562.5	95.8	109	18	US-10-959-318-11
8	562.5	95.8	109	18	US-10-959-318-12
9	561	95.6	110	20	US-11-018-102-23
10	559	95.2	110	20	US-11-018-102-25
11	558	95.1	109	18	US-10-627-556-270

12	557	94.9	110	15	US-10-370-749-23	Sequence 23, Appl
13	557	94.9	110	18	US-10-959-318-1	Sequence 1, Appl
14	557	94.9	110	20	US-11-018-102-22	Sequence 22, Appl
15	553	94.2	109	14	US-10-207-655-220	Sequence 22, Appl
16	553	94.2	109	18	US-10-627-556-14	Sequence 14, Appl
17	553	94.2	110	18	US-10-959-318-4	Sequence 4, Appl
18	553	94.2	110	18	US-10-959-318-21	Sequence 21, Appl
19	553	94.2	110	20	US-11-018-102-24	Sequence 24, Appl
20	552	94.0	109	14	US-10-020-354-80	Sequence 80, Appl
21	552	94.0	110	15	US-10-370-749-53	Sequence 53, Appl
22	550	93.7	110	15	US-10-370-749-51	Sequence 51, Appl
23	550	93.7	110	18	US-10-959-318-22	Sequence 22, Appl
24	549	93.5	109	14	US-10-267-286A-4	Sequence 4, Appl
25	549	93.5	109	18	US-10-627-556-294	Sequence 294, Appl
26	549	93.5	110	18	US-10-959-318-5	Sequence 5, Appl
27	549	93.5	110	18	US-10-959-318-6	Sequence 6, Appl
28	549	93.5	110	18	US-10-959-318-25	Sequence 25, Appl
29	548.5	93.4	109	18	US-10-959-318-15	Sequence 15, Appl
30	548.5	93.4	109	18	US-10-959-318-16	Sequence 16, Appl
31	548	93.4	109	18	US-10-627-556-258	Sequence 258, Appl
32	548	93.4	109	18	US-10-627-556-278	Sequence 278, Appl
33	548	93.4	109	18	US-10-627-556-302	Sequence 302, Appl
34	548	93.4	110	18	US-10-959-318-23	Sequence 23, Appl
35	548	93.4	110	18	US-10-959-318-24	Sequence 24, Appl
36	547	93.2	110	17	US-10-491-653-22	Sequence 22, Appl
37	545	92.8	109	14	US-10-207-655-322	Sequence 322, Appl
38	545	92.8	109	18	US-10-627-556-92	Sequence 92, Appl
39	543.5	92.6	109	18	US-10-959-318-2	Sequence 2, Appl
40	539	91.8	110	18	US-10-959-318-3	Sequence 3, Appl
41	535.5	91.2	109	18	US-10-959-318-17	Sequence 17, Appl
42	535.5	91.2	109	18	US-10-959-318-18	Sequence 18, Appl
43	532	90.6	109	18	US-10-627-556-286	Sequence 286, Appl
44	531	90.5	110	18	US-10-959-318-19	Sequence 19, Appl
45	531	90.5	110	18	US-10-959-318-20	Sequence 20, Appl

#### ALIGNMENTS

RESULT 1  
US-10-959-318-9  
; Sequence 9, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; APPLICANT: Clark, Michael R  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)  
US-10-959-318-9

Query Match 98.6%; Score 579; DB 18; Length 110;  
Best Local Similarity 99.1%; Pred. No. 1.1e-48;  
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APPVAGGSPVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
DB 1 APPVAGGSPVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

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QY 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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Db 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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RESULT 2
US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-10

Query Match 98.6%; Score 579; DB 18; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.1e-48; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 1;

QY 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
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QY 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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Db 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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RESULT 3
US-10-959-318-13
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-13

Query Match 96.3%; Score 565; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 2.4e-47; Indels 0; Gaps 0;
Matches 106; Conservative 1; Mismatches 3;

QY 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
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QY 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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Db 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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RESULT 4
US-10-959-318-14
; Sequence 14, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-14

Query Match 96.3%; Score 565; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 2.4e-47; Indels 0; Gaps 0;
Matches 106; Conservative 1; Mismatches 3;

QY 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
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QY 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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Db 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110
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RESULT 5
US-10-959-318-7
; Sequence 7, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)
; OTHER INFORMATION: mutations
US-10-959-318-13
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QY 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
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QY 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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Db 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110
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RESULT 4
US-10-959-318-14
; Sequence 14, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268)
; OTHER INFORMATION: mutations
US-10-959-318-14

Query Match 96.3%; Score 565; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 2.4e-47; Indels 0; Gaps 0;
Matches 106; Conservative 1; Mismatches 3;

QY 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
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QY 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110
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Db 61 PREEQNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110
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RESULT 5
US-10-959-318-7
; Sequence 7, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)
; OTHER INFORMATION: mutations
US-10-959-318-13
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/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: engineered G1 CH2
US-11-018-102-23

Query Match          95.6%; Score 561; DB 20; Length 110;
Best Local Similarity 95.5%; Pred. No. 6e-47;
Matches 105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APEAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

RESULT 10
US-11-018-102-25
/ Sequence 25, Application US/11018102
/ Publication No. US20050136061A1
/ GENERAL INFORMATION:
/ APPLICANT: Centocor, Inc.
/ TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CEN5045 USA NP
/ CURRENT APPLICATION NUMBER: US/11/018,102
/ CURRENT FILING DATE: 2004-12-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 25
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: engineered G4 CH2
US-11-018-102-25

Query Match          95.2%; Score 559; DB 20; Length 110;
Best Local Similarity 95.5%; Pred. No. 9.4e-47;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APEAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110

RESULT 11
US-10-627-556-270
/ Sequence 270, Application US/10627556
/ Publication No. US20050136049A1
/ GENERAL INFORMATION:
/ APPLICANT: LEDBETTER, JEFFREY A.
/ APPLICANT: HAYDEN-LEDBETTER, MARTHA
/ APPLICANT: THOMPSON, PETER A.
/ TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
/ FILE REFERENCE: 49076.000004.CIP2
/ CURRENT APPLICATION NUMBER: US/10/627,556
/ CURRENT FILING DATE: 2003-07-26
/ PRIOR APPLICATION NUMBER: 10/053,530
/ PRIOR FILING DATE: 2002-01-17
/ PRIOR APPLICATION NUMBER: 60/367,358
/ PRIOR FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 09/765,208
/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 60/385,691
/ PRIOR FILING DATE: 2002-06-03
/ NUMBER OF SEQ ID NOS: 699

/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 270
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-627-556-270

Query Match          95.1%; Score 558; DB 18; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.2e-46;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 61
Db 1 PELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 62 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109

RESULT 12
US-10-370-749-23
/ Sequence 23, Application US/10370749
/ Publication No. US20040002587A1
/ GENERAL INFORMATION:
/ APPLICANT: Watkins, Jeffrey D.
/ APPLICANT: Allan, Barrett
/ TITLE OF INVENTION: FC Region Variants
/ FILE REFERENCE: AMB-07823
/ CURRENT APPLICATION NUMBER: US/10/370,749
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/358,161
/ PRIOR FILING DATE: 2002-02-20
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 23
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ OTHER INFORMATION:
US-10-370-749-23

Query Match          94.9%; Score 557; DB 15; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.5e-46;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

RESULT 13
US-10-959-318-1
/ Sequence 1, Application US/10959318
/ Publication No. US20050215768A1
/ GENERAL INFORMATION:
/ APPLICANT: Armour, Kathryn L
/ APPLICANT: Clark, Michael R
/ TITLE OF INVENTION: Polypeptides including modified constant regions
/ FILE REFERENCE: 39-302
/ CURRENT APPLICATION NUMBER: US/10/959,318
/ CURRENT FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: PCT/GB2004/004254
/ PRIOR FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: GB0324368.0
/ PRIOR FILING DATE: 2003-10-17
/ NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-959-318-1

Query Match

Best Local Similarity 94.9%; Score 557; DB 18; Length 110;

Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 14

US-11-018-102-22

; Sequence 22, Application US/11018102

; Publication No. US20050136061A1

; GENERAL INFORMATION:

; APPLICANT: Centocor, Inc.

; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES

; FILE REFERENCE: CEN5045 USA NP

; CURRENT APPLICATION NUMBER: US/11/018,102

; CURRENT FILING DATE: 2004-12-21

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 22

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-018-102-22

Query Match

Best Local Similarity 94.9%; Score 557; DB 20; Length 110;

Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

Db 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 110

RESULT 15

US-10-207-655-220

; Sequence 220, Application US/10207655

; Publication No. US20030118592A1

; GENERAL INFORMATION:

; APPLICANT: Ledbetter, Jeffrey A.

; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

; FILE REFERENCE: 390069.401C1

; CURRENT APPLICATION NUMBER: US/10/207,655

; CURRENT FILING DATE: 2002-07-25

; NUMBER OF SEQ ID NOS: 426

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 220

; LENGTH: 109

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Fusion polypeptide

US-10-207-655-220

Query Match

94.2%; Score 553; DB 14; Length 109;

Best Local Similarity 94.5%; Pred. No. 3.6e-46;  
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 61  
Db 1 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60  
QY 62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
Db 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 109

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Job time : 83.1279 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 06:38:35 ; Search time 91.6667 Seconds  
(without alignments)  
464.112 Million cell updates/sec

Title: US-09-674-857-12  
Perfect score: 583  
Sequence: 1 APPVAGSPSVLPFPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	97.8	437	7 ADM33855	Adm33855 Human HuE
2	570	97.8	437	8 ADR48986	Adr48986 HuBPO-L-v
3	570	97.8	449	7 ADM33378	Adm33378 Human GCS
4	566.5	97.2	462	2 AAW14933	Aaw14933 2A2 (Chim
5	566.5	97.2	462	2 AAW14934	Aaw14934 2A2 (Chim
6	566.5	97.2	463	2 AAW14939	Aaw14939 3F4 (Chim
7	566.5	97.2	463	2 AAW14940	Aaw14940 3F4 (Chim
8	566.5	97.2	472	5 ABP51695	Abp51695 5G1.1-TP0
9	566.5	97.2	472	8 ADQ16647	Adq16647 Immunoglo
10	565	96.9	110	2 AAR41717	Aar41717 Undefined
11	565	96.9	218	3 AAB07478	Aab07478 Amino aci
12	565	96.9	218	4 AAB76425	Aab76425 Human IGG
13	565	96.9	218	4 AAB67205	Aab67205 Human IGG
14	565	96.9	218	5 AAG78436	Aag78436 Native se
15	565	96.9	218	6 ABR42442	Abr42442 Human IGG
16	565	96.9	218	8 ADH75380	Adh75380 Human IGG
17	565	96.9	229	7 ADD32013	Add32013 Heterolog
18	565	96.9	229	8 ADR48994	Adr48994 Human IGG
19	565	96.9	266	8 ADJ52121	Adj52121 CHI delet
20	565	96.9	284	6 AAE30927	Aae30927 Gly8-Glu2
21	565	96.9	327	2 AAW37346	Aaw37346 Immunoglo
22	565	96.9	327	5 AAM47859	Aam47859 Human IGG
23	565	96.9	327	6 AAE32918	Aae32918 Human imm
24	565	96.9	327	6 AAE32630	Aae32630 Human imm
25	565	96.9	327	6 AAO30892	Aao30892 Human imm

26	565	96.9	327	7 ADE97357	Ade97357 Human IGG
27	565	96.9	327	7 ADF75004	Adf75004 Human Ig
28	565	96.9	327	8 ADMA1543	Adma1543 Anti-inte
29	565	96.9	329	2 AAW70801	Aaw70801 Amino aci
30	565	96.9	329	3 AAY92190	Aay92190 Human IGG
31	565	96.9	329	7 ABW02169	Abw02169 Human Cga
32	565	96.9	329	8 ADL35097	Adl35097 Human IGG
33	565	96.9	330	6 ABR42735	Abr42735 Anti-ties
34	565	96.9	382	2 AAR90922	Aar90922 IL4.Y124D
35	565	96.9	382	2 AAR90921	Aar90921 IL4.Y124D
36	565	96.9	396	2 AAW10534	Aaw10534 Leptin 1-
37	565	96.9	396	2 AAW10535	Aaw10535 Leptin 1-
38	565	96.9	403	7 ADD32018	Add32018 Heterolog
39	565	96.9	432	2 AAY17903	Aay17903 Human IFN
40	565	96.9	433	2 AAW18579	Aaw18579 Interfero
41	565	96.9	443	2 AAW13564	Aaw13564 Human IGG
42	565	96.9	444	2 AAY31672	Aay31672 Human IGG
43	565	96.9	444	6 ABR55342	Abr55342 Amino aci
44	565	96.9	444	7 ADC73234	Adc73234 Protein s
45	565	96.9	444	8 ADF69629	Adf69629 Humanized

ALIGNMENTS

RESULT 1  
ADM33855  
ID ADM33855 standard; protein; 437 AA.

XX AC ADM33855;

XX 03-JUN-2004 (first entry)

XX Human HuBPO-L-vFcgamma4 fusion protein.

XX Erythropoietin; EPO; immunoglobulin; IGG;  
KW fragment crystallisation region; Fc; chronic anaemia; renal disease;  
KW cancer chemotherapy; rheumatoid arthritis; AIDS;  
KW myelodysplastic syndrome; (HuEPO)-L-vFcgamma4; human.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..27 /note= "Signal peptide"

FT Protein 28..192 /note= "Linker"

FT Peptide 193..208 /note= "EPO"

FT Protein 209..437 /note= "IgG4 Fc"

FT Misc-difference 219 /note= "Wild-type Ser substituted by Pro"

FT Misc-difference 226 /note= "Wild-type Leu substituted by Ala"

US2003082749-A1.

PD 01-MAY-2003.

XX 17-AUG-2001; 2001US-00932812.

XX 17-AUG-2001; 2001US-00932812.

XX (SUNL/) SUN L K.

XX (SUNB/) SUN B N C.

XX (SUNC/) SUN C R Y.

XX Sun LK, Sun BNC, Sun CRV;

XX WPI; 2003-616080/58.

DR N-PSDB; ADM33854.



QY 1 APPVAGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 60  
|||  
Db 221 APEFAGGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 280  
|||  
QY 61 PREOFNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110  
|||  
Db 281 PREOFNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 330  
|||

RESULT 3  
ADM33378  
ID ADM33378 standard; protein; 449 AA.  
XX AC ADM33378;  
XX DT 03-JUN-2004 (first entry)  
XX DE Human GCSF-L-fragment of crystallisation gamma 4 fusion protein.  
XX cytotatic; immunostimulant; antianaemic; anti-HIV; protein therapy;  
KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-VFC;  
KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;  
KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;  
KW bone marrow transplantation; chronic neutropenia; fusion protein;  
KW fragment of crystallisation gamma 4; Fc gamma 4.  
XX Homo sapiens.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Misc-difference 228 /note= "Wild type Ser substituted by Pro"  
FT Misc-difference 235 /note= "Wild type Leu substituted by Ala"  
FT  
FT  
FT  
XX US2003082679-A1.  
XX 01-MAY-2003.  
XX 01-OCT-2001; 2001US-00968362.  
XX 01-OCT-2001; 2001US-00968362.  
XX (SUNL/) SUN L K.  
XX (SUNB/) SUN B N C.  
XX (SUNC/) SUN C R Y.  
XX Sun LK, Sun BNC, Sun CRY;  
XX WPI; 2003-585400/55.  
XX N-PSDB; ADM33377.  
XX New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-  
PT vfc fusion protein for treating immune or hematopoietic system disorders  
PT comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G  
PT Fc variant.  
XX  
XX Disclosure; Fig 2B; 15pp; English.  
XX The invention describes a recombinant human granulocyte colony-  
CC stimulating factor (hG-CSF)-L-VFC fusion protein comprising hG-CSF, a  
CC peptide linker, and a human immunoglobulin G (IgG) Fc variant. Also  
CC described are: a CHO-derived cell line producing the above hG-CSF-L-VFC  
CC fusion protein in its growth medium in excess of 10 mg/g per million  
CC cells in a 24-hour period; and making the recombinant fusion protein  
CC cited above, comprising generating a CHO-derived cell line cited above,  
CC growing the cell line under conditions the recombinant fusion protein is  
CC expressed in its growth medium, and purifying the expressed protein. The  
CC recombinant fusion protein is useful in treating a variety of conditions  
CC associated with an impaired immune or hematopoietic system, including  
CC cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow  
CC transplantation, and chronic neutropenias. This is the amino acid

CC sequence of human GCSF-L-fragment of crystallisation gamma 4 variant  
CC fusion protein.  
XX  
SQ Sequence 449 AA;  
Query Match 97.8%; Score 570; DB 7; Length 449;  
Best Local Similarity 98.2%; Pred. No. 8.2e-49; Mismatches 2; Indels 0; Gaps 0;  
Matches 108; Conservative 0;  
QY 1 APPVAGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 60  
|||  
Db 233 APEFAGGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATK 292  
|||  
QY 61 PREOFNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 110  
|||  
Db 293 PREOFNSTYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTISKAK 342  
|||

RESULT 4  
AAW14933  
ID AAW14933 standard; protein; 462 AA.  
XX AC AAW14933;  
XX DT 17-OCT-2003 (revised)  
DT 16-JUN-1997 (first entry)  
XX DE 2A2 (Chimeric) human G2/G4 chimeric antibody.  
XX Xenotransplantation; graft rejection; cell interaction; pig;  
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
KW chimeric antibody; diagnosis.  
XX Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX WO9711971-A1.  
XX 03-APR-1997.  
XX 27-SEP-1996; 96WO-US015575.  
XX 28-SEP-1995; 95US-0004489P.  
XX 26-SEP-1996; 96US-00004489.  
XX (ALEX-) ALEXION PHARM INC.  
XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;  
PI WPI; 1997-212855/19.  
XX N-PSDB; AAT62931.  
XX Antibodies binding to porcine but not human cell interaction proteins -  
PT useful to treat and assay for rejection of xenografted porcine organs,  
PT tissues or cells.  
XX  
XX Disclosure; Page 42-44; 105pp; English.  
XX A chimeric antibody (AAW14933) comprises the C1 and hinge regions of  
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAB) and a  
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)  
CC monoclonal antibody (MAB) 2A2 heavy chain variable region sequence (see  
CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is  
CC useful for diagnosing human rejection of porcine xenotransplants and for  
CC improving xenotransplantation of porcine cells, tissues and organs into  
CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 462 AA;  
Query Match 97.2%; Score 566.5; DB 2; Length 462;  
Best Local Similarity 99.1%; Pred. No. 1.9e-48; Mismatches 0; Indels 1; Gaps 1;  
Matches 109; Conservative 0;

```

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 247 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 305

QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110
DB 306 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 355

RESULT 5
AAW14934
ID AAW14934 standard; protein; 462 AA.
XX
AC AAW14934;
XX
DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
XX
DE 2A2 (Chimeric) human G2/G4 chimeric antibody.
XX
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX
PN WO9711971-A1.
XX
PD 03-APR-1997.
XX
PF 27-SEP-1996; 96WO-US015575.
XX
PR 28-SEP-1995; 95US-0004489P.
PR 26-SEP-1996; 96US-00004489.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
DR WPI; 1997-212855/19.
DR N-PSDB; AAT62932.
XX
PT Antibodies binding to porcine but not human cell interaction proteins -
PT useful to treat and assay for rejection of xenografted porcine organs,
PT tissues or cells.
XX
PS Disclosure; Page 44-47; 105pp; English.
XX
CC A chimeric antibody (AAW14934) comprises the C1 and hinge regions of
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC monoclonal antibody (Mab) 2A2 heavy chain variable region sequence (see
CC also AAW14932). The chimeric antibody is specific for porcine VCAM. It is
CC useful for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs into
CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 462 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 462;
Best Local Similarity 99.1%; Pred. No. 1.9e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 247 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 305

QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110
DB 306 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 355

```

```

RESULT 6
AAW14939
ID AAW14939 standard; protein; 463 AA.
XX
AC AAW14939;
XX
DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
XX
DE 3F4 (Chimeric) human G2/G4 chimeric antibody.
XX
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX
PN WO9711971-A1.
XX
PD 03-APR-1997.
XX
PF 27-SEP-1996; 96WO-US015575.
XX
PR 28-SEP-1995; 95US-0004489P.
PR 26-SEP-1996; 96US-00004489.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;
DR WPI; 1997-212855/19.
DR N-PSDB; AAT62936.
XX
PT Antibodies binding to porcine but not human cell interaction proteins -
PT useful to treat and assay for rejection of xenografted porcine organs,
PT tissues or cells.
XX
PS Disclosure; Page 56-57; 105pp; English.
XX
CC A chimeric antibody (AAW14939) comprises the C1 and hinge regions of
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC monoclonal antibody (Mab) 3F4 heavy chain variable region sequence (see
CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
CC useful for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs into
CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 463 AA;

Query Match 97.2%; Score 566.5; DB 2; Length 463;
Best Local Similarity 99.1%; Pred. No. 1.9e-48;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
DB 248 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 306

QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110
DB 307 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 356

RESULT 7
AAW14940
ID AAW14940 standard; protein; 463 AA.
XX
AC AAW14940;
XX

```

DT 17-OCT-2003 (revised)  
 XX 16-JUN-1997 (first entry)  
 DE 3F4 (Chimeric) human G2/G4 chimeric antibody.  
 XX Xenotransplantation; graft rejection; cell interaction; pig;  
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
 KW chimeric antibody; diagnosis.  
 XX Homo; sapiens.  
 OS Mus sp.  
 OS Chimeric.  
 XX WO9711971-A1.  
 XX 03-APR-1997.  
 XX 27-SEP-1996; 96WO-US015575.  
 XX 28-SEP-1995; 95US-0004489P.  
 PR 26-SEP-1996; 96US-00004489.  
 XX (ALEX-) ALEXION PHARM INC.  
 XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;  
 XX WPI; 1997-212855/19.  
 DR N-PSDB; AAT62937.  
 XX Antibodies binding to porcine but not human cell interaction proteins -  
 PT useful to treat and assay for rejection of xenografted porcine organs,  
 PT tissues or cells.  
 XX Disclosure; Page 58-61; 105pp; English.  
 XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of  
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a  
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)  
 CC monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see  
 CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is  
 CC useful for diagnosing human rejection of porcine xenotransplants and for  
 CC improving xenotransplantation of porcine cells, tissues and organs into  
 CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 463 AA;  
 Query Match 97.2%; Score 566.5; DB 2; Length 463;  
 Best Local Similarity 99.1%; Pred. No. 1.9e-48;  
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 APPVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
 DB 248 APPVA-GPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 306  
 QY 61 PREQFNSTYRVSVLTIVLHODWLNCKEYKCKVSNKGLPSSIEKTIKAK 110  
 DB 307 PREQFNSTYRVSVLTIVLHODWLNCKEYKCKVSNKGLPSSIEKTIKAK 356  
 RESULT 8  
 ABP51695  
 ID ABP51695 standard; protein; 472 AA.  
 XX  
 AC ABP51695;  
 XX  
 DT 01-OCT-2002 (first entry)  
 DE SG1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.  
 XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;  
 KW complementarity determining region; immunoglobulin; antianaemic;  
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.  
 XX

OS Homo sapiens.  
 XX Synthetic.  
 XX WO200246238-A2.  
 XX 13-JUN-2002.  
 XX 05-DEC-2001; 2001WO-US047656.  
 XX 05-DEC-2000; 2000US-0251448P.  
 PR 04-MAY-2001; 2001US-0288889P.  
 PR 29-MAY-2001; 2001US-0294068P.  
 XX (ALEX-) ALEXION PHARM INC.  
 XX Bowdish KS, Barbas-Frederickson S, Renshaw M;  
 XX WPI; 2002-566610/60.  
 DR N-PSDB; ABQ73374.  
 XX A novel immunogen molecule comprising a region in which amino acid  
 PT residues corresponding to at least a portion of the complementary  
 PT determining region are replaced or fused with an erythropoietin or  
 PT thrombopoietin mimetic.  
 XX Example 4; Fig 13A; 113pp; English.  
 XX The present invention describes an immunoglobulin molecule or its fragment  
 CC (I) comprising a region where amino acid residues corresponding to at  
 CC least a portion of the complementary determining region (CDR) are  
 CC replaced or fused with biologically active peptides e.g. a peptide  
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,  
 CC that is flanked with proline at its carboxy terminus. (I) has  
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as  
 CC a stimulator of proliferation, differentiation and maturation of  
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful  
 CC for stimulating proliferation, differentiation or growth of  
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with  
 CC promegakaryocytes or megakaryocytes, which results in increased platelet  
 CC production. (I) with a region where amino acid residues corresponding to  
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or  
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the  
 CC production of red blood cells, where (I) is contacted with haematopoietic  
 CC stem cells or their progenitors. (I) is useful for diagnostics or  
 CC therapeutics, in cell isolation strategies, and for treating patients  
 CC suffering from deficiency in cell populations caused by disease,  
 CC disorders or treatments related to the suppression of haematopoiesis.  
 CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 472 AA;  
 Query Match 97.2%; Score 566.5; DB 5; Length 472;  
 Best Local Similarity 99.1%; Pred. No. 2e-48;  
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 APPVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
 DB 257 APPVA-GPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315  
 QY 61 PREQFNSTYRVSVLTIVLHODWLNCKEYKCKVSNKGLPSSIEKTIKAK 110  
 DB 316 PREQFNSTYRVSVLTIVLHODWLNCKEYKCKVSNKGLPSSIEKTIKAK 365  
 RESULT 9  
 ADQ16647  
 ID ADQ16647 standard; protein; 472 AA.  
 XX  
 AC ADQ16647;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX

DE	Immunoglobulin antibody 5G1.1-TPO heavy chain SEQ ID NO:67.
XX	
KW	immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KW	erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KW	immunotherapy; thrombocytopenia.
XX	
OS	Synthetic.
XX	
PN	WO2004050017-A2.
XX	
PD	17-JUN-2004.
XX	
PF	17-NOV-2003; 2003WO-US036894.
XX	
PR	02-DEC-2002; 2002US-00307724.
XX	
PA	(ALEX-) ALEXION PHARM INC.
XX	
PI	Bowdish KS, Frederickson S, Renshaw M;
XX	
DR	WPI; 2004-460973/43.
DR	N-PSDB; ADQ16648.
XX	
PT	New immunoglobulin molecule comprising a region, where two
PT	complementarity determining regions (CDRs) are replaced with EPO mimetic
PT	or a TPO mimetic, useful for treating thrombocytopenia.
XX	
PS	Example 4; SEQ ID NO 67; 107pp; English.
XX	
CC	The invention relates to a novel immunoglobulin molecule or its fragment
CC	comprising a region where amino acid residues corresponding to at least a
CC	portion of a two complementarity determining regions (CDRs) are replaced
CC	with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC	a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC	invention has immunosuppressive activity, and may have a use in
CC	immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC	treating thrombocytopenia as a result of chemotherapy, bone marrow
CC	transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC	The present sequence represents an immunoglobulin antibody heavy chain of
CC	the invention.
XX	
SQ	Sequence 472 AA;
<p>Query Match 97.2%; Score 566.5; DB 8; Length 472;</p> <p>Best Local Similarity 99.1%; Pred. No. 2e-48;</p> <p>Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1</p>	
QY	1 APPVAGPSVFLFPKPKDTLMSRTPVTCVVVDVSDQDPVQFNWYDGVVHNAKTK 60
DB	257 APPVA-GPSVFLFPKPKDTLMSRTPVTCVVVDVSDQDPVQFNWYDGVVHNAKTK 315
QY	61 PREEQFNSTYRVVSVLTVLHQLWLNKGYCKVSNKGLPSSIEKTIISKAK 110
DB	316 PREEQFNSTYRVVSVLTVLHQLWLNKGYCKVSNKGLPSSIEKTIISKAK 365
RESULT 10	
AAR41717	ID AAR41717 standard; protein; 110 AA.
XX	AAR41717;
XX	25-MAR-2003 (revised)
DT	20-OCT-1993 (first entry)
XX	Undefined ORF2 encoded by plasmid pAH4808.
XX	
KW	Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
KW	light; chain; variable; constant; region; anti-human; pAH4807;
KW	transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW	endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
KW	diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW	Parkinsons disease; Alzheimers disease; SP2/0 cell.



PF 14-JAN-2000; 2000WO-US000973.  
 XX  
 PR 15-JAN-1999; 99US-0116023P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX Presta LG;  
 PI  
 XX WPI; 2000-476035/41.  
 XX  
 XX New Fc region-containing polypeptides that have altered effector function  
 PT due to one or more amino acid modifications in the Fc region, useful in  
 PT the treatment of cancer and allergic conditions such as asthma.  
 XX  
 XX Disclosure; Fig 22A; 132pp; English.  
 XX  
 CC AAB07474-78 represent native IgG Fc regions. The proteins are used to  
 CC produce Fc region-containing polypeptides that have altered effector  
 CC function as a consequence of one or more amino acid modifications in the  
 CC Fc region. The variant polypeptides are useful for treating cancer,  
 CC allergic conditions such as asthma (with an anti-IgE antibody), and LFA-1  
 CC -mediated disorders. Where the polypeptide binds the HER2 receptor, the  
 CC disorder preferably is HER2-expressing cancer, e.g. a benign or malignant  
 CC tumour characterized by overexpression of the HER2 receptor. Such cancers  
 CC include breast cancer, squamous cell cancer, small-cell lung cancer, non-  
 CC small cell lung cancer, gastrointestinal cancer, pancreatic cancer,  
 CC glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma,  
 CC colon cancer, colorectal cancer, endometrial carcinoma, salivary gland  
 CC carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer,  
 CC thyroid cancer, hepatic carcinoma and various types of head and neck  
 CC cancer  
 XX  
 SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 3; Length 218;  
 Best Local Similarity 97.3%; Pred. No. 1.1e-48;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
 |||  
 DB 2 APFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61  
 |||  
 QY 61 PREEQFNSTYRVSVLTFLVTHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 |||  
 DB 62 PREEQFNSTYRVSVLTFLVTHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 111  
 |||

RESULT 12  
 AAB76425  
 ID AAB76425 standard; protein; 218 AA.  
 XX  
 AC AAB76425;  
 XX  
 XX 10-APR-2001 (first entry)  
 DT  
 DE Human IgG4 Fc region amino acid sequence.  
 XX  
 XX Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia;  
 KW metabolic disorder; nutritional deficiency; Alzheimer's disease;  
 KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;  
 KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200101748-A2.  
 PN  
 XX 11-JAN-2001.  
 PD  
 XX 30-JUN-2000; 2000WO-US018283.  
 PF  
 XX 02-JUL-1999; 99US-0142232P.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA

XX Dennis MS;  
 PI  
 XX WPI; 2001-123048/13.  
 DR  
 XX Non-naturally occurring peptide ligands which compete for binding human  
 PT erbB2 gene products, useful for treating e.g. Alzheimer's disease,  
 PT multiple sclerosis and diabetic neuropathy.  
 PT  
 XX Disclosure; Fig 2A; 116pp; English.  
 PS  
 XX This invention relates to non-naturally occurring peptide ligands which  
 CC bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides  
 CC represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples  
 CC of the ErbB2 binding ligands of the invention. Sequences AAB76421 -  
 CC AAB76431 represent antibody Fc amino acid sequences used in the isolation  
 CC of the peptides of the invention. The peptides compete for binding ErbB2  
 CC with naturally occurring ligands, and may be used to treat disorders  
 CC characterized by over expression of HER2/erbB2 such as cancers, diseases  
 CC of the nervous system, musculature and epithelia, e.g. nervous system  
 CC damage resulting from trauma, surgery, strokes, ischaemia, infection,  
 CC metabolic disorders, nutritional deficiency or toxic agents. In  
 CC particular the synthetic peptide ligands may be used to treat Alzheimer's  
 CC disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's  
 CC chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy  
 CC associated with diabetes  
 XX  
 SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 4; Length 218;  
 Best Local Similarity 97.3%; Pred. No. 1.1e-48;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
 |||  
 DB 2 APFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61  
 |||  
 QY 61 PREEQFNSTYRVSVLTFLVTHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 |||  
 DB 62 PREEQFNSTYRVSVLTFLVTHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 111  
 |||

RESULT 13  
 AAB67205  
 ID AAB67205 standard; protein; 218 AA.  
 XX  
 AC AAB67205;  
 XX  
 XX 10-APR-2001 (first entry)  
 DT  
 DE Human IgG4.  
 XX  
 XX Fusion protein; immunoglobulin; multidimerization domain; ligand.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200102440-A1.  
 PN  
 XX 11-JAN-2001.  
 PD  
 XX 30-JUN-2000; 2000WO-US018185.  
 PF  
 XX 02-JUL-1999; 99US-0142088P.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Dennis MS, Lazarus RA;  
 PI  
 XX WPI; 2001-123106/13.  
 DR  
 XX Novel fusion polypeptides comprising a peptide ligand domain which  
 PT functions to target hybrid molecule to target cell, and immunoglobulin  
 PT constant region multimerization domain.

XX Disclosure; Fig 2; 69pp; English.

XX The present invention relates to a fusion protein, comprising a peptide

CC ligand and an immunoglobulin (Ig) constant region multimerization domain

CC (1b). The hybrid molecules comprising the peptide ligands and their

CC functional derivatives can be used in the same applications as, a peptide

CC ligand can be used. For example the peptide ligand can bind ErbB2. The

CC peptide ligand may bind to and inhibit the activity associated with a

CC particular target molecule

XX Sequence 218 AA;

SQ

Query Match 96.9%; Score 565; DB 4; Length 218;

Best Local Similarity 97.3%; Pred. No. 1.1e-48;

Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

DB 2 APEFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 61

QY 61 PREEQFNSTYRVVSVLTVTLHQLDNLGKEYKCKVSNKGLPSSIEKTTISKAK 110

DB 62 PREEQFNSTYRVVSVLTVTLHQLDNLGKEYKCKVSNKGLPSSIEKTTISKAK 111

RESULT 14

AAG78436

ID AAG78436 standard; protein; 218 AA.

XX AAG78436;

XX

XX 12-APR-2002 (first entry)

XX Native sequence human IgG Fc region sequence humIgG4.

XX Antibody; antigen; immunoglobulin; ADCC; CDC; anti-globin response;

KW antibody dependant cell mediated cytotoxicity;

KW complement dependant cytotoxicity; epidermal growth factor receptor;

KW tumour necrosis factor; lymphocyte; tetraivalent antibody; cytostatic;

KW antiinflammatory; antipapillary; dermatological; anticancer;

KW antiasthmatic; antiarteriosclerotic; antirheumatic; antibacterial;

KW antiarthritic; neuroprotective; immunosuppressive; antianaemic;

KW antiallergic; antidiabetic; gene therapy; human.

XX Homo sapiens.

XX

XX WO200177342-A1.

XX

XX 18-OCT-2001.

XX

XX 20-MAR-2001; 2001WO-US008928.

XX

XX 11-APR-2000; 2000US-0195819P.

XX

XX (GETH ) GENENTECH INC.

XX

XX Miller KL, Presta LG;

XX

XX WPI; 2002-049149/06.

XX

XX Novel engineered antibody useful in therapeutic applications, contains a

PT dimerization domain and three or more antigen binding sites.

XX

XX Disclosure; Fig 3; 186pp; English.

XX This invention relates to an isolated antibody comprising a dimerisation

CC domain and three or more antigen binding sites amino-terminal to the

CC domain. It is cytostatic, antiinflammatory, antibacterial,

CC immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used

CC in gene therapy. Along with a cytotoxic agent, is useful for treating a

CC disorder e.g. cancer in a mammal, for inducing apoptosis of a cancer

CC cell, and for killing a B cell or a cell which overexpresses or expresses

CC an ErbB receptor and for treating benign and malignant tumours,

CC inflammatory, angiogenic and immunological disorders, autoimmune

CC diseases, central nervous system inflammatory disorders. The antibody is

CC also useful for immunodiagnosis of various diseases including cancer, for

CC human therapy in redirected cytotoxicity, and also useful as fibrinolytic

CC agents or vaccine adjuvants, useful as affinity purification agent, in

CC diagnostic assays for detecting the expression of antigen of interest in

CC specific cells, tissue or serum, and useful for blocking an immune

CC response to a foreign antigen. The antigen is internalised faster than a

CC bivalent antibody by a cell expressing an antigen to which the antibodies

CC bind. The antibody comprises three or four heavy chain variable domains

CC which are able to combine with three or four light chain variable domain

CC polypeptides to form three or four antigen binding sites directed against

CC the same antigen. This sequence represents the native sequence human IgG

CC Fc region, humIgG4

XX

SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 5; Length 218;

Best Local Similarity 97.3%; Pred. No. 1.1e-48;

Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60

DB 2 APEFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 61

QY 61 PREEQFNSTYRVVSVLTVTLHQLDNLGKEYKCKVSNKGLPSSIEKTTISKAK 110

DB 62 PREEQFNSTYRVVSVLTVTLHQLDNLGKEYKCKVSNKGLPSSIEKTTISKAK 111

RESULT 15

ABR42442

ID ABR42442 standard; protein; 218 AA.

XX ABR42442;

XX

XX 11-AUG-2003 (first entry)

XX Human IgG4 Fc region.

DE Human IgG4 Fc region.

XX

KW Human; antibody; IgG4; cytostatic; immunosuppressive; antiinflammatory;

KW antimicrobial.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

FH Misc-difference 153

FT /note= "given as 'Z' in Fig 23"

XX

XX WO2003035835-A2.

XX

XX 01-MAY-2003.

XX

XX 22-OCT-2002; 2002WO-US033739.

XX

XX 25-OCT-2001; 2001US-0337642P.

PR 09-JAN-2002; 2002US-0347694P.

XX

XX (GETH ) GENENTECH INC.

XX

XX Presta LG;

XX

XX WPI; 2003-421411/39.

XX

XX New composition comprising a glycoprotein having a Fc region useful for

PT treating cancer, autoimmune disease, inflammatory disorder or infection

PT in a mammal.

XX

XX Disclosure; Fig 23; 139pp; English.

XX

XX The present sequence is the protein sequence of the Fc region of human

CC IgG4. A claimed composition comprises a glycoprotein having a Fc region.

CC About 80-100% of the glycoprotein comprises a mature core carbohydrate  
CC structure which lacks fucose attached to the Fc region. The glycoprotein  
CC preferably comprises an antibody, and the Fc region is preferably a human  
CC IgG Fc region, especially a human IgG1, IgG2, IgG3 or IgG4 Fc region. The  
CC glycoprotein binds FcγRIII with better affinity, or mediates antibody  
CC -dependent cell-mediated cytotoxicity more effectively, than the  
CC glycoprotein including fucose. The antibody may be chimeric, humanised or  
CC human and binds a B-cell surface marker, an ErbB receptor, a tumour-  
CC associated antigen or an angiogenic factor, CD20, HER2, vascular  
CC endothelial growth factor, CD40 or prostate stem cell antigen. The  
CC composition is useful for treating cancer, autoimmune disease, an  
CC inflammatory disorder or infection in a mammal  
XX  
SQ Sequence 218 AA;

Query Match 96.9%; Score 565; DB 6; Length 218;  
Best Local Similarity 97.3%; Pred. No. 1.le-48;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2 APEFLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61  
Qy 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 110  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
62 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTIISKAK 111

Search completed: November 17, 2005, 07:04:57  
Job time : 93.6667 secs

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:49:37 ; Search time 18.0822 Seconds  
(without alignments)  
585.319 Million cell updates/sec

Title: US-09-674-857-12  
Perfect score: 583  
Sequence: 1 APPVAGGPSVFLPPPKPKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.9	327	1 G4HU	Ig gamma-4 chain C
2	542.5	93.1	326	1 G2HU	Ig gamma-2 chain C
3	541	92.8	234	2 PT0207	Ig gamma chain C r
4	541	92.8	255	4 S31866	Ig gamma-1 chain C
5	541	92.8	330	1 GHU	Ig gamma-1 chain C
6	541	92.8	374	2 S69339	Ig heavy chain V r
7	531	91.1	377	2 A23511	Ig gamma-3 chain C
8	531	91.1	377	2 A60764	Ig gamma-3 chain C
9	518	88.9	289	1 G3HUI	Ig gamma-3 heavy C
10	470	80.6	328	2 I47160	Ig gamma 2b chain
11	470	80.6	328	2 I47159	Ig gamma 2a chain
12	465	79.8	277	2 I47162	Ig gamma 4 chain C
13	443	76.0	328	2 I47161	Ig gamma 3 chain C
14	443	76.0	328	2 I47158	Ig gamma 1 chain C
15	433	74.3	308	2 C30554	Ig heavy chain C r
16	433	74.3	323	1 GHRB	Ig gamma chain C r
17	433	74.3	333	2 PS0018	Ig gamma-2b chain
18	433	74.3	472	2 S31459	Ig gamma-1 chain -
19	431	73.9	470	2 S22080	Ig heavy chain pre
20	426	73.1	329	1 G2GP	Ig gamma-2 chain C
21	417	71.5	329	1 G3MSC	Ig gamma-3 chain C
22	417	71.5	328	1 G3MSM	Ig gamma-3 chain C
23	409	70.2	327	2 S06611	Ig gamma-2 chain C
24	405	69.5	324	1 G1MS	Ig gamma-1 chain C
25	405	69.5	393	1 G1MSM	Ig gamma-1 chain C
26	405	69.5	444	2 PC4436	monoclonal antibod
27	403	69.1	329	2 S00847	Ig gamma-2c chain
28	399	68.4	405	1 G2MSBM	Ig gamma-2b chain
29	399	68.4	474	1 G2MS11	Ig gamma-2b chain

30 396 67.9 335 1 G2MSAB Ig gamma-2a chain  
31 393 67.4 330 1 G2MSA Ig gamma-2a chain  
32 393 67.4 399 1 G2MSAM Ig gamma-2a chain  
33 393 67.4 469 2 S37483 Ig gamma-2a chain  
34 389 66.7 326 2 PS0017 Ig gamma-1 chain C  
35 385 66.0 475 2 S01321 Ig gamma-2b chain  
36 383 65.7 446 2 S40295 Ig gamma-2a chain  
37 343 58.8 322 2 PS0019 Ig gamma-2a chain  
38 311 53.3 112 2 B30503 Ig gamma-2a chain  
39 278 47.7 88 2 A30503 Ig gamma-2b chain  
40 258 44.3 180 2 I46732 Ig gamma heavy cha  
41 167.5 28.7 426 2 I36948 Ig epsilon-chain -  
42 166.5 28.6 428 1 EHHU Ig epsilon chain C  
43 165 28.3 152 2 S14236 Ig gamma-1 chain C  
44 154 26.4 549 2 S04845 Ig heavy chain pre  
45 151 25.9 429 1 EHRT Ig epsilon chain C

ALIGNMENTS

RESULT 1  
G4HU  
Ig gamma-4 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
C;Accession: A90933; A90249; A02150  
R;Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A;Reference number: A90933; MUID:83157104; PMID:6299662  
A;Accession: A90933  
A;Molecule type: DNA  
A;Residues: 1-327 <ELL>  
A;Cross-references: UNIPROT:P01861  
A;Note: the sequence was determined from the germline gene  
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A;Title: Human immunoglobulin C region; immunoglobulin homology  
A;Reference number: A90249; MUID:70207560; PMID:4192699  
A;Accession: A90249  
A;Molecule type: protein  
A;Residues: 1-30;81-326 <PIN>  
C;Genetics:  
A;Gene: GDB:IGHG4  
A;Cross-references: GDB:119340; OMIM:147130  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 111/1; 221/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;99-110/Region: hinge  
F;134-203/Domain: immunoglobulin homology <IM2>  
F;240-307/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83,141-201,247-305/Disulfide bonds: #status predicted  
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;177/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 96.9%; Score 565; DB 1; Length 327;  
Best Local Similarity 97.3%; Pred. No. 6;3e-49;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDVGVHNATK 60  
Db 111 APEFLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDVGVHNATK 170  
Qy 61 PREEQNSYRVVSVLTVHLQDWLNKGYCKVSNKGLPSSIEKTSKAK 110  
Db 171 PREEQNSYRVVSVLTVHLQDWLNKGYCKVSNKGLPSSIEKTSKAK 220



Db 99 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 148

# RESULT 5

GHUU

Ig gamma-1 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004

C/Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146

R/Elison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; MUID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <ELL>

A/Cross-references: UNIPROT:P01857; EMBL:Z17370

A/Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,

A/Note: Lys-330 is removed after translation

R/Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A/Reference number: S33887; MUID:83001943; PMID:6811139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A/Reference number: A90563; MUID:71064024; PMID:5489771

A/Contents: myeloma protein Eu

A/Accession: B90563

A/Molecule type: Protein

A/Residues: 1-96,'R',98-135 <CUN>

A/Note: this sequence has the G1m(3) marker, 97-Arg

R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A/Reference number: A90564; MUID:71064025; PMID:5530842

A/Contents: Eu

A/Accession: A90564

A/Molecule type: Protein

A/Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A/Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R/Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A/Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.

A/Reference number: A91668; MUID:77070269; PMID:826475

A/Contents: myeloma protein Nie

A/Accession: B91668

A/Molecule type: protein

A/Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27

A/Note: this sequence has the G1m(17) and G1m(1) markers

R/Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A/Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI

A/Reference number: A91723; MUID:83289131; PMID:6884994

A/Contents: myeloma protein KOI; disulfide bonds

A/Accession: A91723

A/Molecule type: protein

A/Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH

A/Note: this sequence has the G1m(3) and G1m(non-1) markers

R/Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid

A/Reference number: A90565; MUID:71064027; PMID:4923144

A/Contents: annotation; disulfide bonds

R/Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

enbromide cleavage products, and the disulfide bridges

A/Reference number: A91667; MUID:77070267; PMID:11002129

A/Contents: annotation; disulfide bonds

C/Genetics:

A/Gene: GDB:IGHG1

A/Cross-references: GDB:120085; OMIM:147100

A/Map position: 14q32.33-14q32.33

A/Introns: 99/1; 114/1; 224/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology <IM1>

F/137-206/Domain: immunoglobulin homology <IM2>

F/243-310/Domain: immunoglobulin homology <IM3>

F/27-83,144-204,250-308/Disulfide bonds: #status experimental

F/103/Disulfide bonds: interchain (to light chain) #status experimental

F/109,112/Disulfide bonds: interchain (to heavy chain) #status experimental

F/180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 92.8%; Score 541; DB 1; Length 330;

Best Local Similarity 91.8%; Pred. No. 1.6e-46;

Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLPPPKDLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNATK 60

Db 114 APBLGGPSVFLPPPKDLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNATK 173

Qy 61 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110

Db 174 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPAPIEKTISKAK 223

# RESULT 6

S69339

Ig heavy chain V region precursor - human

C/Species: Homo sapiens (man)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000

C/Accession: S69339; S72664

R/Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A/Reference number: S69339; MUID:95262687; PMID:7744049

A/Accession: S69339

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-374 <KHA>

A/Cross-references: EMBL:X81695

R/Khamilichi, A.A.

submitted to the EMBL Data Library, September 1994

A/Reference number: S72664

A/Accession: S72664

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-140,'C',142-374 <KH2>

A/Cross-references: EMBL:X81695

C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 92.8%; Score 541; DB 2; Length 374;

Best Local Similarity 91.8%; Pred. No. 1.9e-46;

Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLPPPKDLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNATK 60

Db 158 APBLGGPSVFLPPPKDLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNATK 217

Qy 61 PREEQNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110





C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47160  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
C;Accession: I47160  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126  
C;Genetics:  
A;Gene: Igc2b  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;133-202/Domain: immunoglobulin homology <IMM>  
  
Query Match 80.6%; Score 470; DB 2; Length 328;  
Best Local Similarity 81.7%; Pred. No. 2e-39;  
Matches 85; Conservative 12; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 7 GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVGVHNAKTKPREEQF 66  
Db 116 GPSVFIFPPPKDGLMISRTPEVTCVVVDVSQENPEVQFSWYVDGVGVHNAKTRKKEQF 175  
  
Qy 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
Db 176 NSTYRVSVLPIQHODWLNGKEFKCKVNNKDLPAITRIISKAK 219  
  
RESULT 11  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47159  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
C;Accession: I47159  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
C;Genetics:  
A;Gene: Igc2a  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;133-202/Domain: immunoglobulin homology <IMM>  
  
Query Match 80.6%; Score 470; DB 2; Length 328;  
Best Local Similarity 81.7%; Pred. No. 2e-39;  
Matches 85; Conservative 12; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 7 GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVGVHNAKTKPREEQF 66  
Db 116 GPSVFIFPPPKDGLMISRTPEVTCVVVDVSQENPEVQFSWYVDGVGVHNAKTRKKEQF 175  
  
Qy 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
Db 176 NSTYRVSVLPIQHODWLNGKEFKCKVNNKDLPAITRIISKAK 219  
  
RESULT 12  
I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47162  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47162  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-277 <KAC>  
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130  
C;Genetics:  
A;Gene: Igc4  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;82-151/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.8%; Score 465; DB 2; Length 277;  
Best Local Similarity 80.8%; Pred. No. 5.2e-39;  
Matches 84; Conservative 12; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 7 GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVGVHNAKTKPREEQF 66  
Db 65 GPSAFIFPPPKDGLMISRTPEVTCVVVDVSQENPEVQFSWYVDGVGVHNAKTRKKEQF 124  
  
Qy 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110  
Db 125 NSTYRVSVLPIQHODWLNGKEFKCKVNNKDLPAITRIISKAK 168  
  
RESULT 13  
I47161  
Ig gamma 3 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47161  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
C;Accession: I47161  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128  
C;Genetics:  
A;Gene: Igc3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;133-202/Domain: immunoglobulin homology <IMM>  
  
Query Match 76.0%; Score 443; DB 2; Length 328;  
Best Local Similarity 78.6%; Pred. No. 1e-36;  
Matches 81; Conservative 12; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 7 GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVGVHNAKTKPREEQF 66  
Db 116 GPSVFIFPPPKDGLMISRTPEVTCVVVDVSQENPEVQFSWYVDGVGVHNAKTRKKEQF 175  
  
Qy 67 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109  
Db 176 NSTYRVSVLPIQHODWLNGKEFKCKVNNKDLPAITRIISKAK 218  
  
RESULT 14  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47158  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
C;Accession: I47158  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122  
C;Genetics:  
A;Gene: Igc1

C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match           76.0%; Score 443; DB 2; Length 328;  
Best Local Similarity 78.6%; Pred.No.le-36;  
Matches         81; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY      7 GPSVFLEPPPKPDTLMISRPETVTCVVVDVSQEDPEVQFNWYDGVGVEVHNAKTKPRREQF 66  
        | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db      116 GPVSFIPLPPPKPDTLMISQTPEVTCCVVVDVSKHAEVQFSWYDGVGEVHTAETRKPEEQF 175  
        | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY      67 NSITRVSVSLTVLHDWLNGKEYCKCVSNKGFLPSLSIEKTISK 109  
        | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Db      176 NSTVRVSVSLPIQHODLVLGKEFKCFKNVNDLPAPITRTISKA 218  
        | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 15

C30554  
Ig heavy chain C region - sheep (fragment)  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 03-Mar-1989 #sequence\_revision 03-Mar-1989 #text\_change 21-Jan-2000  
C/Accession: C30554  
R/Foley, R.C.; Beh, K.J.  
J. Immunol. 142, 708-711, 1989  
A/Rittle: Isolation and sequence of sheep Ig H and L chain cDNA.  
A/Reference number: A30554; MUID:89093962; PMID:2492052  
A/Accession: C30554  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-308 <POL>  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/113-182/Domain: immunoglobulin homology <IMM>

[illegible]

Search completed: November 17, 2005, 07:11:38  
Job time : 19.0822 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:47:37 ; Search time 80.6164 Seconds  
(without alignments)  
698.725 Million cell updates/sec

Title: US-09-674-857-12  
Perfect score: 583  
Sequence: 1 APPVAGPSVLPFPKPKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	565	96.9	327	1	GC4_HUMAN
2	565	96.9	473	2	Q8TC63
3	562	96.4	476	2	Q6MZX7
4	542.5	93.1	326	1	GC2_HUMAN
5	542.5	93.1	417	2	Q6N093
6	542.5	93.1	465	2	Q6P6C4
7	541	92.8	330	1	GC1_HUMAN
8	541	92.8	348	2	Q6PYX1
9	541	92.8	465	2	Q6GMX6
10	541	92.8	466	2	Q6IN78
11	541	92.8	469	2	Q7Z7P5
12	541	92.8	470	2	Q6PJ44
13	541	92.8	470	2	Q7Z5W1
14	541	92.8	472	2	Q6N089
15	541	92.8	473	2	Q6MZV7
16	541	92.8	473	2	Q6P055
17	541	92.8	475	2	Q6GMW7
18	541	92.8	475	2	Q6MZQ6
19	541	92.8	475	2	Q6N095
20	541	92.8	476	2	Q6GMX1
21	541	92.8	478	2	Q6P181
22	541	92.8	480	2	Q6N094
23	541	92.8	480	2	Q6PJF1
24	541	92.8	481	2	Q6N097
25	541	92.8	482	2	Q7Z3S1
26	541	92.8	544	2	Q6PJ95
27	541	92.8	679	2	Q96PQ8
28	539.5	92.5	464	2	Q6MZU6
29	538	92.3	466	2	Q6N096
30	536	91.9	487	2	Q652L2
31	534	91.6	509	2	Q8NF17

32	534	91.6	521	2	Q8N4Y9
33	533.5	91.5	493	2	Q68CN4
34	531	91.1	354	2	Q86TT2
35	531	91.1	518	2	Q6N030
36	518	88.9	290	1	GC3_HUMAN
37	462	79.2	337	2	Q95M34
38	433	74.3	323	1	GC_RABIT
39	433	74.3	333	1	GC_B_RAT
40	426	73.1	329	1	GC2_CAVPO
41	417	71.5	303	2	Q6KAM2
42	417	71.5	329	1	GC3_MOUSE
43	417	71.5	398	1	GC3M_MOUSE
44	417	71.5	470	2	Q7TWK1
45	405	69.5	324	1	GC1_MOUSE

ALIGNMENTS

RESULT 1	GC4_HUMAN	STANDARD;	PRT;	327 AA.
ID	GC4_HUMAN			
AC	P01861;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	IG gamma-4 chain C region.			
GN	Name=IGHG4;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83157104; PubMed=6299662;			
RA	Ellison J.W., Buxbaum J.N., Hood L.E.;			
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";			
RL	DNA 1:11-18(1981).			
RN	[2]			
RP	SEQUENCE OF 1-30 AND 81-326.			
RX	MEDLINE=7027560; PubMed=4192699;			
RA	Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;			
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the			
RL	Biochem. J. 117:33-47(1970).			
CC				
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CC	or send an email to license@isb-sib.ch).			
CC				
DR	EMBL; K01316; AAB59394.1; ALT_INIT.			
DR	PIR; A90933; G4HU.			
DR	PDB; 1ADQ; X-ray; A=118-323.			
DR	Genew; HGNC:5528; IGHG4.			
DR	MIM; 147130; .			
DR	GO; GO:0005624; C:membrane fraction; NAS.			
DR	GO; GO:0003823; F:antigen binding; TAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	PFam; PF00047; ig; 3.			
DR	SMART; SM00407; IGC1; 2.			
DR	PROSITE; PS00835; IG_LIKE; 3.			
DR	PROSITE; PS00290; IG_MHC; 2.			
KW	3D-structure; Direct protein sequencing; Immunoglobulin C region;			
KW	Immunoglobulin domain			
FT	NON_TER 1 98			
FT	DOMAIN 1 98 CHI.			

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FT DOMAIN 99 110 Hinge.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 Interchain (with a light chain).
FT DISULFID 27 83
FT DISULFID 106 106 Interchain (with a heavy chain).
FT DISULFID 109 109 Interchain (with a heavy chain).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 96.9%; Score 565; DB 1; Length 327;
Best Local Similarity 97.3%; Pred. No. 3.9e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 60
Db 111 APEFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 170

QY 61 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 171 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 220

RESULT 2
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
PFam; PF07654; C1-set; 3.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 96.9%; Score 565; DB 2; Length 473;
Best Local Similarity 97.3%; Pred. No. 5.9e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 60
Db 257 APEFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 316

QY 61 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 317 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 366

RESULT 3
Q6MZK7 PRELIMINARY; PRT; 476 AA.
AC Q6MZK7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686M24218.
GN Name=DKFZp686M24218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640824; CAE45900.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
PFam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FFE5853958F CRC64;

Query Match 96.4%; Score 562; DB 2; Length 476;
Best Local Similarity 96.4%; Pred. No. 1.2e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 60
Db 260 APEFLGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNAKTK 319

QY 61 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 320 PREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIISKAK 369

RESULT 4
GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE IG gamma-2 chain C region.  
GN Name=IGHG2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellison J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy  
chain constant region genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=83001943; PubMed=6329676;  
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for  
evolution of a gene family.";  
RL Cell 29:671-679(1982).  
RN [3]  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
genes.";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
evolutionary, and functional implications.";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=80001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
domains of a human IgG2 myeloma protein.";  
RL Can. J. Biochem. 57:758-767(1979).  
RN [6]  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;  
RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
immunoglobulin gamma chains.";  
RL Mol. Immunol. 16:923-925(1979).  
RN [7]  
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
RA Hofmann T., Parr D.M.;  
RL Submitted (MAR-1980) to the PIR data bank.  
RN [8]  
RP SEQUENCE OF 1-121 (DOT).  
RX MEDLINE=9525298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
immunoglobulins.";  
RL Eur. J. Biochem. 228:886-893(1995).  
RN [9]  
RP DISULFIDE BONDS.  
RX MEDLINE=72033500; PubMed=4940472;  
RA Milstein C., Frangione B.;  
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
RL Biochem. J. 121:217-225(1971).  
RN [10]  
RP DISULFIDE BONDS.  
RX MEDLINE=69064124; PubMed=5782707;

RA Frangione B., Milstein C., Pink J.R.L.;  
RT "Structural studies of immunoglobulin G.";  
RL Nature 221:145-148(1969).  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00230; AAB59393.1; --  
DR PIR; A93906; G2HU.  
DR HSSP; P01857; IOQX.  
DR Genew; HGNC:5526; IGHG2.  
DR MIM; 147110; --  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGH1; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Direct protein sequencing; Immunoglobulin C region;  
KW Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 Hinge.  
FT DOMAIN 111 219 CH2.  
FT DOMAIN 220 326 CH3.  
FT DISULFID 14 14 Interchain (with a light chain).  
FT DISULFID 27 83 Interchain (with a heavy chain).  
FT DISULFID 102 102 Interchain (with a heavy chain).  
FT DISULFID 103 103 Interchain (with a heavy chain).  
FT DISULFID 106 106 Interchain (with a heavy chain).  
FT DISULFID 109 109 Interchain (with a heavy chain).  
FT DISULFID 140 200  
FT DISULFID 246 304  
FT SITE 156 156  
FT VARIANT 60 60  
FT CONFLICT 109 109 At or near the complement-binding site.  
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;  
SQ  
Query Match 93.1%; Score 542.5; DB 1; Length 326;  
Best Local Similarity 93.6%; Pred. No. 6.9e-46;  
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 APPVAGGVSFLPPPKKDTLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNAKTK 60  
Db 111 APPVA-GPSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNAKTK 169  
Qy 61 PREEQNSTYRVVSVLTITVLQDWMNGKEYKCKVSNKGLPSSIEKTIKAK 110  
Db 170 PREEQNSTYRVVSVLTITVLQDWMNGKEYKCKVSNKGLPAPIKTISKTK 219  
RESULT 5  
Q6N093 PRELIMINARY; PRT; 417 AA.  
ID Q6N093  
AC Q6N093;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686I04196 (Fragment).  
GN Name=DKFZp686I04196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA The German Human cDNA Consortium;
RG Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640623; CAB45777.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; PS00835; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 417 AA; 46061 MW; C4518B844CFB883C CRC64;

Query Match 93.1%; Score 542.5; DB 2; Length 417;
Best Local Similarity 93.6%; Pred. No. 9.1e-46;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTK 60
DB 202 APPVA-GPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTK 260
QY 61 PREEQNSTFRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
DB 261 PREEQNSTFRVSVLTVLHQDLNGKEYCKVSNKGLPAPIEKTSKTK 310

RESULT 6
Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD89348ADC37B6D CRC64;

Query Match 93.1%; Score 542.5; DB 2; Length 465;
Best Local Similarity 93.6%; Pred. No. 1e-45;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTK 60
DB 250 APPVA-GPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTK 308
QY 61 PREEQNSTFRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTSKAK 110
DB 309 PREEQNSTFRVSVLTVLHQDLNGKEYCKVSNKGLPAPIEKTSKTK 358

RESULT 7
GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name-IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
```

RA Ponstingl H., Hilschmann N.;  
 RT "The rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic  
 RT peptides of the H-chain, alignment of the tryptic peptides and  
 RT discussion of the complete structure.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).  
 RP [5]  
 RN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
 RX MEDLINE=83289131; PubMed=684994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RT "Three-dimensional structure determination of antibodies. Primary  
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).  
 RP [6]  
 RN DISULFIDE BONDS.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196 (1970).  
 RP [7]  
 RN DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).  
 RP [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370 (1981).  
 CC -!- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC GIM(3) marker and the GIM (non-1) markers.  
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
 DR PIR; A93433; GHHU.  
 DR PDB; 1AJ7; X-ray; H=1-103.  
 DR PDB; 1DSB; X-ray; B/H=1-101.  
 DR PDB; 1DS1; X-ray; H=1-101.  
 DR PDB; 1D6V; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1E4K; X-ray; A/B=106-329.  
 DR PDB; 1FCL; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCC; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I7Z; X-ray; B/D=1-103.  
 DR PDB; 1IIS; X-ray; A/B=107-330.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1OQX; X-ray; A/B=119-330.  
 DR PDB; 1AJ7; X-ray; H=1-103.  
 DR PDB; 1DSB; X-ray; B/H=1-101.  
 DR PDB; 1DS1; X-ray; H=1-101.  
 DR PDB; 1D6V; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1E4K; X-ray; A/B=106-329.  
 DR PDB; 1FCL; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCC; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I7Z; X-ray; B/D=1-103.  
 DR PDB; 1IIS; X-ray; A/B=107-330.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1OQX; X-ray; A/B=119-330.

DR PDB; 2RCS; X-ray; H=1-103.  
 DR Genew; HGNC:5525; IGHL1.  
 DR MIM; 147100; -.  
 DR GO; GO:0005624; C-membrane fraction; NAS.  
 DR GO; GO:0003823; F-antigen binding; TAS.  
 DR GO; GO:0006955; P-immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct\_protein sequencing; Glycoprotein;  
 KW Immunoglobulin C region; Immunoglobulin domain.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CHI.  
 FT DOMAIN 99 110 Hinge.  
 FT DOMAIN 111 223 CH2.  
 FT DOMAIN 224 330 CH3.  
 FT DISULFID 27 83  
 FT DISULFID 103 103 Interchain (with light chain).  
 FT DISULFID 109 109 Interchain (with heavy chain).  
 FT DISULFID 112 112 Interchain (with heavy chain).  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT CARBOHYD 180 180  
 FT VARIANT 97 97 N-linked (GlcNAc...).  
 FT VARIANT 239 239 K -> R (in GIM(3) marker).  
 FT VARIANT 241 241 /FTid=VAR\_003886.  
 FT VARIANT 241 241 D -> E (in GIM(non-1) marker).  
 FT VARIANT 241 241 /FTid=VAR\_003887.  
 FT VARIANT 241 241 L -> M (in GIM(non-1) marker).  
 FT VARIANT 241 241 /FTid=VAR\_003888.  
 FT STRAND 23 24  
 FT STRAND 26 33  
 FT STRAND 38 38  
 FT STRAND 41 41  
 FT TURN 42 45  
 FT TURN 48 49  
 FT STRAND 50 52  
 FT STRAND 57 58  
 FT TURN 59 61  
 FT STRAND 62 71  
 FT HELIX 73 75  
 FT TURN 76 78  
 FT STRAND 82 87  
 FT TURN 88 91  
 FT STRAND 92 97  
 FT TURN 102 103  
 FT STRAND 122 126  
 FT TURN 130 134  
 FT TURN 136 137  
 FT STRAND 141 149  
 FT STRAND 157 162  
 FT TURN 163 164  
 FT STRAND 165 167  
 FT STRAND 171 172  
 FT STRAND 176 177  
 FT TURN 179 180  
 FT STRAND 183 190  
 FT HELIX 193 197  
 FT TURN 198 199  
 FT STRAND 202 207  
 FT TURN 209 210  
 FT STRAND 215 219  
 FT STRAND 227 227  
 FT STRAND 230 234  
 FT HELIX 238 242  
 FT STRAND 245 256  
 FT STRAND 261 266  
 FT TURN 267 268  
 FT STRAND 269 270  
 FT STRAND 274 276  
 FT STRAND 280 281  
 FT TURN 283 284

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FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 311
FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770BE106C2FA33D CRC64;

Query Match 92.8%; Score 541; DB 1; Length 330;
Best Local Similarity 91.8%; Pred. No. 9.9e-46;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60
Db 114 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 173

QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 174 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAK 223

RESULT 8
Q6PYX1 ID Q6PYX1 PRELIMINARY; PRT; 348 AA.
AC Q6PYX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; AY570731; AAS88328.1; -.
RA HSP; P01857; 1A77.
RA GO; GO:0004872; F:receptor activity; IEA.
RA InterPro; IPR007110; Ig-like.
RA InterPro; IPR003597; Ig cl.
RA InterPro; IPR003006; Ig_MHC.
RA Pfam; PF07654; Cl-set; 3.
RA SMART; SM00407; IGcl; 3.
RA PROSITE; PSS0835; IG_LIKE; 3.
RA PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Receptor.
FT NON TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;

Query Match 92.8%; Score 541; DB 2; Length 348;
Best Local Similarity 91.8%; Pred. No. 1.1e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60
Db 132 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 191

QY 61 PREEQFNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 192 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAK 241

RESULT 9
Q6GMX6 ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC073766; AAH73766.1; -.
RA InterPro; IPR003599; Ig.
RA InterPro; IPR007110; Ig-like.
RA InterPro; IPR003597; Ig cl.
RA InterPro; IPR003006; Ig_MHC.
RA InterPro; IPR003596; Ig_v.
RA Pfam; PF07654; Cl-set; 3.
RA Pfam; PF00047; Ig; 4.
RA SMART; SM00409; IG; 2.
RA SMART; SM00407; IGcl; 3.
RA SMART; SM00406; Igv; 1.
RA PROSITE; PSS0835; IG_LIKE; 4.
RA PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 92.8%; Score 541; DB 2; Length 465;
Best Local Similarity 91.8%; Pred. No. 1.5e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60
Db 249 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 308

QY 61 PREEQFNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIISKAK 110
Db 309 PREEQNSTYRVSVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAK 358

RESULT 10
Q6IN78 ID Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 92.8%; Score 541; DB 2; Length 470;
Best Local Similarity 91.8%; Pred. No. 1.5e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 60
Db 254 APPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 313

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVKSNKGLPSSIEKTSKAK 110
Db 314 PREEQNSTYRVSVLTVLHODWLNKGYCKVKSNKGLPSSIEKTSKAK 363

RESULT 13
Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 92.8%; Score 541; DB 2; Length 470;
Best Local Similarity 91.8%; Pred. No. 1.5e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 60
Db 254 APPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVGVHNAKTK 313

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVKSNKGLPSSIEKTSKAK 110
Db 314 PREEQNSTYRVSVLTVLHODWLNKGYCKVKSNKGLPSSIEKTSKAK 363

RESULT 14
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AC Q6N089
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.

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Job time : 80.6164 secs

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OM protein - protein search, using sw model

Run on: November 17, 2005, 06:51:22 ; Search time 24.6119 Seconds  
(without alignments)  
333.636 Million cell updates/sec

Title: US-09-674-857-12  
Perfect score: 583  
Sequence: 1 APPVAGGPSVFLPPPKPOT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: Issued Patents AA:\*
  - 2: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	565	96.9	110	3	US-08-444-644-44
3	565	96.9	110	3	US-08-232-246A-44
4	565	96.9	218	4	US-09-483-588-7
5	565	96.9	229	4	US-09-968-362A-28
6	565	96.9	327	2	US-08-761-277A-47
7	565	96.9	329	4	US-09-313-942-12
8	565	96.9	382	1	US-08-470-299-7
9	565	96.9	382	1	US-08-470-299-10
10	565	96.9	443	5	PCT-US96-13152-4
11	565	96.9	467	1	US-08-704-744-81
12	565	96.9	467	2	US-07-916-098A-45
13	565	96.9	467	3	US-08-523-894-8
14	565	96.9	467	3	US-08-523-894-10
15	565	96.9	467	3	US-08-523-894-12
16	561	96.2	109	2	US-08-070-116A-4
17	561	96.2	109	2	US-08-557-050-4
18	559	95.9	326	3	US-08-808-720-3
19	559	95.9	326	4	US-09-467-638-3
20	559	95.9	328	3	US-08-808-720-1
21	559	95.9	328	4	US-09-467-638-1
22	559	95.9	331	3	US-08-808-720-5
23	559	95.9	331	3	US-08-808-720-7
24	559	95.9	331	4	US-09-467-638-5
25	559	95.9	331	4	US-09-467-638-7
26	559	95.9	374	4	US-09-227-595-26
27	559	95.9	374	4	US-09-227-595-28

28	559	95.9	374	4	US-08-595-590B-26	Sequence 26, Appl
29	559	95.9	374	4	US-08-595-590B-28	Sequence 28, Appl
30	554	95.0	447	4	US-09-968-362A-22	Sequence 22, Appl
31	547.5	93.9	448	4	US-09-968-362A-18	Sequence 18, Appl
32	546	93.7	468	3	US-09-485-737B-67	Sequence 67, Appl
33	546	93.7	468	4	US-10-071-485-67	Sequence 67, Appl
34	546	93.7	488	4	US-09-499-846-12	Sequence 12, Appl
35	546	93.7	497	4	US-09-499-846-10	Sequence 10, Appl
36	546	93.7	525	3	US-09-485-737B-90	Sequence 90, Appl
37	546	93.7	711	3	US-10-071-485-90	Sequence 90, Appl
38	546	93.7	711	4	US-08-444-644-30	Sequence 30, Appl
39	542.5	93.1	109	3	US-08-232-246A-30	Sequence 30, Appl
40	542.5	93.1	109	3	US-09-483-588-5	Sequence 5, Appl
41	542.5	93.1	217	4	US-09-968-362A-27	Sequence 27, Appl
42	542.5	93.1	228	4	US-08-477-460B-2	Sequence 2, Appl
43	542.5	93.1	432	3	US-08-379-516-2	Sequence 2, Appl
44	542.5	93.1	432	3	US-09-329-916-2	Sequence 2, Appl
45	542.5	93.1	432	3		

ALIGNMENTS

RESULT 1  
US-09-968-362A-20  
; Sequence 20, Application US/09968362A  
; Patent No. 6797493  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
; FILE REFERENCE: 03SUN2001  
; CURRENT APPLICATION NUMBER: US/09/968,362A  
; CURRENT FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 20  
; TYPE: PRT  
; LENGTH: 449  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hG-CSP-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2  
; OTHER INFORMATION: B)  
US-09-968-362A-20

Query Match	97.8%	Score	570;	DB	4;	Length	449;
Best Local Similarity	98.2%	Pred. No.	2.2e-60;				
Matches	108;	Conservative	0;	Mismatches	2;	Indels	0;
Gaps	0;						
Qy	1	APPVAGGPSVFLPPPKPOTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK	60				
Db	233	APPVAGGPSVFLPPPKPOTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK	292				
Qy	61	PREEQNSYRVVSVLTVHLQDMLNKEYCKVKNKGLPSSIEKTISKAK	110				
Db	293	PREEQNSYRVVSVLTVHLQDMLNKEYCKVKNKGLPSSIEKTISKAK	342				

RESULT 2  
US-08-444-644-44  
; Sequence 44, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive

```
/ CITY: Lexington
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02173
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 07-JUL-1994
/ APPLICATION NUMBER: US 08/232,246
/ PRIOR APPLICATION DATA:
/ FILING DATE: 07-SEP-1990
/ APPLICATION NUMBER: PCT/US90/05077
/ FILING DATE: 07-SEP-1989
/ APPLICATION NUMBER: US 07/800,458
/ FILING DATE: 26-NOV-1991
/ APPLICATION NUMBER: PCT/US90/05077
/ FILING DATE: 07-SEP-1990
/ APPLICATION NUMBER: PCT/US90/05077
/ FILING DATE: 07-SEP-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wagner, Richard W.
/ REGISTRATION NUMBER: 34,480
/ REFERENCE/DOCKET NUMBER: ALK88-15AAA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 861-6240
/ TELEFAX: (617) 861-9540
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 110 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-444-644-44

Query Match          96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
QY 61 PREEQFNSTYRVSVVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQFNSTYRVSVVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 3
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; MEDIUM TYPE: Floppy disk

/ CITY: Lexington
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02173
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 07-JUL-1994
/ APPLICATION NUMBER: US 08/232,246
/ PRIOR APPLICATION DATA:
/ FILING DATE: 07-SEP-1990
/ APPLICATION NUMBER: PCT/US90/05077
/ FILING DATE: 07-SEP-1989
/ APPLICATION NUMBER: US 07/800,458
/ FILING DATE: 26-NOV-1991
/ APPLICATION NUMBER: PCT/US90/05077
/ FILING DATE: 07-SEP-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wagner, Richard W.
/ REGISTRATION NUMBER: 34,480
/ REFERENCE/DOCKET NUMBER: ALK88-15AAA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 861-6240
/ TELEFAX: (617) 861-9540
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 110 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-444-644-44

Query Match          96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
QY 61 PREEQFNSTYRVSVVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQFNSTYRVSVVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110

RESULT 4
US-09-483-588-7
; Sequence 7, Application US/09483588
; Patent No. 6737056
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
; FILE REFERENCE: P1726R1
; CURRENT APPLICATION NUMBER: US/09/483,588
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: US 60/116,023
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-483-588-7

Query Match          96.9%; Score 565; DB 4; Length 218;
Best Local Similarity 97.3%; Pred. No. 3.4e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 2 APEFLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61
QY 61 PREEQFNSTYRVSVVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAK 110
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Db 62 PREEQFNSTYRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 111
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RESULT 5
US-09-968-362A-28
; Sequence 28, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Human IgG4 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-28

Query Match 96.9%; Score 565; DB 4; Length 229;
Best Local Similarity 97.3%; Pred. No. 3.6e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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Db 13 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 72
|||||
Qy 61 PREEQFNSTYRVSVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110
|||||
Db 73 PREEQFNSTYRVSVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 122
|||||

RESULT 6
US-08-761-277A-47
; Sequence 47, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOP-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
```

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; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-761-277A-47

Query Match 96.9%; Score 565; DB 2; Length 327;
Best Local Similarity 97.3%; Pred. No. 5.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|||
Db 111 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170
|||||
Qy 61 PREEQFNSTYRVSVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110
|||||
Db 171 PREEQFNSTYRVSVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 220
|||||

RESULT 7
US-09-313-942-12
; Sequence 12, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-12

Query Match 96.9%; Score 565; DB 4; Length 329;
Best Local Similarity 97.3%; Pred. No. 5.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
|||
Db 113 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 172
|||||
Qy 61 PREEQFNSTYRVSVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 110
|||||
Db 173 PREEQFNSTYRVSVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTISKAK 222
|||||

RESULT 8
US-08-470-299-7
; Sequence 7, Application US/08470299
; Patent No. 5783181
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael J.
; APPLICANT: Murphy, Kay E.
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Clinkenbeard, Helen E.
; APPLICANT: Young, Peter R.
; APPLICANT: Shatzman, Allan R.
; TITLE OF INVENTION: No. 5783181el Compounds
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
```

/ CITY: King of Prussia  
/ STATE: Pennsylvania  
/ COUNTRY: USA  
/ ZIP: 19406  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/470,299  
/ FILING DATE: 06-JUN-1995  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Sutton, Jeffrey A.  
/ REGISTRATION NUMBER: 34,028  
/ REFERENCE/DOCKET NUMBER: P31005C3  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 610-270-5024  
/ TELEFAX: 610-270-5090  
/ INFORMATION FOR SEQ ID NO: 7:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 382 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear  
/ US-08-470-299-7

Query Match 96.9%; Score 565; DB 1; Length 382;  
Best Local Similarity 97.3%; Pred. No. 7.3e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 166 APEFLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225  
  
QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110  
DB 226 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 275

RESULT 9  
US-08-470-299-10  
/ Sequence 10, Application US/08470299  
/ Patent No. 5783181  
/ GENERAL INFORMATION:  
/ APPLICANT: Browne, Michael J.  
/ APPLICANT: Murphy, Kay E.  
/ APPLICANT: Chapman, Conrad G.  
/ APPLICANT: Clinkenbeard, Helen E.  
/ APPLICANT: Young, Peter R.  
/ APPLICANT: Shatzman, Allan R.  
/ TITLE OF INVENTION: No. 5783181el Compounds  
/ NUMBER OF SEQUENCES: 21  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: SmithKline Beecham Corporation  
/ STREET: 709 Swedeland Road, P.O. Box 1539  
/ CITY: King of Prussia  
/ STATE: Pennsylvania  
/ COUNTRY: USA  
/ ZIP: 19406  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/470,299  
/ FILING DATE: 06-JUN-1995  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Sutton, Jeffrey A.  
/ REGISTRATION NUMBER: 34,028

/ REFERENCE/DOCKET NUMBER: P31005C3  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 610-270-5024  
/ TELEFAX: 610-270-5090  
/ INFORMATION FOR SEQ ID NO: 10:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 382 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear  
/ US-08-470-299-10

Query Match 96.9%; Score 565; DB 1; Length 382;  
Best Local Similarity 97.3%; Pred. No. 7.3e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
DB 166 APEFEGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225  
  
QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 110  
DB 226 PREEQFNSTYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAK 275

RESULT 10  
PCT-US96-13152-4  
/ Sequence 4, Application PC/TUS9613152  
/ GENERAL INFORMATION:  
/ APPLICANT: Martin, Ulrich, et al.  
/ TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai  
/ NUMBER OF SEQUENCES: 4  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Felte & Lynch  
/ ADDRESSEE: Attn: Norman D. Hanson  
/ STREET: 805 Third Avenue  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: U.S.A.  
/ ZIP: 10022  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Computer Disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: ASCII  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US96/13152  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION NUMBER: 08/578,953  
/ FILING DATE: 27-Dec-95  
/ APPLICATION NUMBER: EP 95 112 895.8  
/ FILING DATE: 17-Aug-95  
/ APPLICATION NUMBER: EP 95 114 969.9  
/ FILING DATE: 19-Sep-95  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Norman D. Hanson  
/ REGISTRATION NUMBER: 30,946  
/ REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 688-9200  
/ TELEFAX: (212) 838-3884  
/ INFORMATION FOR SEQ ID NO: 4:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 443  
/ TYPE: amino acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ PCT-US96-13152-4

Query Match 96.9%; Score 565; DB 5; Length 443;



Best Local Similarity 97.3%; Pred. No. 8.9e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
|||  
Db 227 APEFLGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 286  
|||

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
|||  
Db 287 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 336  
|||

RESULT 11  
US-08-704-744-81  
; Sequence 81, Application US/08704744  
; Patent No. 5705154  
; GENERAL INFORMATION:  
; APPLICANT: Dalie, Barbara  
; APPLICANT: Miller, Kenneth  
; APPLICANT: Murgolo, Nicholas  
; APPLICANT: Tindall, Stephen  
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schering-Plough Corporation  
; STREET: 2000 Galloping Hill Road  
; CITY: Kenilworth  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07033-0530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.5.3  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/704,744  
; FILING DATE: 06-SEPT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/208886  
; FILING DATE: 10-MAR-1994  
; APPLICATION NUMBER: PCT/US/95/02400  
; FILING DATE: 08-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Foulke, Cynthia L.  
; REGISTRATION NUMBER: 32,364  
; REFERENCE/DOCKET NUMBER: JB0429K  
; TELEPHONE: (908) 298-2987  
; TELEFAX: (908) 298-5388  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 81:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-704-744-81

Query Match 96.9%; Score 565; DB 1; Length 467;  
Best Local Similarity 97.3%; Pred. No. 9.5e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
|||  
Db 251 APEFLGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310  
|||

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
|||  
Db 311 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 360  
|||

Best Local Similarity 97.3%; Pred. No. 8.9e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
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Db 252 APEFLGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 311  
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QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
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Db 312 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 361  
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RESULT 12  
US-07-916-098A-45  
; Sequence 45, Application US/07916098A  
; Patent No. 5871732  
; GENERAL INFORMATION:  
; APPLICANT: BURKLY, LINDA C.  
; APPLICANT: CHISHOLM, PATRICIA L.  
; APPLICANT: THOMAS, DAVID W.  
; APPLICANT: ROSA, MARGARET D.  
; APPLICANT: ROSA, JOSEPH J.  
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
; STREET: 10 SOUTH WACKER DRIVE  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: U.S.A.  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/916,098A  
; FILING DATE: July 24, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/08843  
; FILING DATE: No. 5871732ember 27, 1991  
; CLASSIFICATION: 424  
; APPLICATION NUMBER: 07/618,542  
; FILING DATE: No. 5871732ember 27, 1990  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JOHN J. MC DONNELL  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92,310-G  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 715-1000  
; TELEFAX: (312) 715-1234  
; TELEX: 910/221-5317  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-916-098A-45

Query Match 96.9%; Score 565; DB 2; Length 467;  
Best Local Similarity 97.3%; Pred. No. 9.5e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
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Db 252 APEFLGSPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 311  
|||

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110  
|||  
Db 312 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 361  
|||

RESULT 13  
US-08-523-894-8  
; Sequence 8, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.

;/ TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
;/ TITLE OF INVENTION: Therapy  
;/ NUMBER OF SEQUENCES: 59  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
;/ STREET: 699 Prince Street  
;/ CITY: Alexandria  
;/ STATE: VA  
;/ COUNTRY: USA  
;/ ZIP: 22314-3187  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/523,894  
;/ FILING DATE: 06-SEP-1995  
;/ CLASSIFICATION: 424  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Teskin, Robin L.  
;/ REGISTRATION NUMBER: 35,030  
;/ REFERENCE/DOCKET NUMBER: 012712-165  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 703-836-6620  
;/ TELEFAX: 703-836-2021  
;/ INFORMATION FOR SEQ ID NO: 8:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 467 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ US-08-523-894-8

Query Match 96.9%; Score 565; DB 3; Length 467;  
Best Local Similarity 97.3%; Pred. No. 9.5e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 251 APEFLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310  
QY 61 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 311 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 360

RESULT 14  
US-08-523-894-10  
; Sequence 10, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/523,894  
; FILING DATE: 06-SEP-1995

;/ CLASSIFICATION: 424  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Teskin, Robin L.  
;/ REGISTRATION NUMBER: 35,030  
;/ REFERENCE/DOCKET NUMBER: 012712-165  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 703-836-6620  
;/ TELEFAX: 703-836-2021  
;/ INFORMATION FOR SEQ ID NO: 10:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 467 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ US-08-523-894-10

Query Match 96.9%; Score 565; DB 3; Length 467;  
Best Local Similarity 97.3%; Pred. No. 9.5e-60;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db 251 APEFEGGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310  
QY 61 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 311 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 360

RESULT 15  
US-08-523-894-12  
; Sequence 12, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/523,894  
; FILING DATE: 06-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
;/ US-08-523-894-12

Query Match 96.9%; Score 565; DB 3; Length 467;  
Best Local Similarity 97.3%; Pred. No. 9.5e-60;

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Db	251	APEPEGGSPVELFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK	310							
Qy	61	PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	110							
Db	311	PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	360							

Search completed: November 17, 2005, 07:13:22  
Job time : 24.6119 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 07:05:08 ; Search time 84.3836 Seconds  
(without alignments)  
545.427 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 593

Sequence: 1 APPVAGGPSVFLPPPKPKPT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	98.8	110	18	US-10-959-318-9
2	573	98.3	110	18	US-10-959-318-10
3	571	97.9	110	20	US-11-018-102-25
4	570	97.8	437	10	US-09-932-812-20
5	570	97.8	437	16	US-10-761-593A-20
6	570	97.8	437	20	US-11-016-518A-20
7	570	97.8	437	20	US-11-017-185-20
8	570	97.8	449	10	US-09-968-362-20
9	570	97.8	449	16	US-10-800-497-20
10	570	97.8	449	16	US-10-800-449-20
11	566.5	97.2	472	14	US-10-006-593-67

12	566.5	97.2	472	15	US-10-307-724-67	Sequence 67, Appl
13	566.5	97.2	472	16	US-10-737-290-67	Sequence 67, Appl
14	565	96.9	110	18	US-10-959-318-4	Sequence 4, Appl
15	565	96.9	110	20	US-11-018-102-24	Sequence 24, Appl
16	565	96.9	218	9	US-09-813-341-5	Sequence 5, Appl
17	565	96.9	218	14	US-10-277-370-5	Sequence 5, Appl
18	565	96.9	218	14	US-10-196-394-76	Sequence 76, Appl
19	565	96.9	218	15	US-10-370-749-18	Sequence 18, Appl
20	565	96.9	218	16	US-10-835-642-7	Sequence 7, Appl
21	565	96.9	218	16	US-10-757-863-7	Sequence 7, Appl
22	565	96.9	218	17	US-10-982-470-7	Sequence 7, Appl
23	565	96.9	218	17	US-11-158-839-7	Sequence 7, Appl
24	565	96.9	219	16	US-10-704-406-6	Sequence 6, Appl
25	565	96.9	229	16	US-10-761-593A-28	Sequence 28, Appl
26	565	96.9	229	16	US-10-800-497-28	Sequence 28, Appl
27	565	96.9	229	16	US-10-800-449-28	Sequence 28, Appl
28	565	96.9	229	20	US-11-016-518A-28	Sequence 28, Appl
29	565	96.9	229	20	US-11-017-185-28	Sequence 28, Appl
30	565	96.9	266	18	US-10-609-783B-51	Sequence 51, Appl
31	565	96.9	284	15	US-10-433-108-24	Sequence 24, Appl
32	565	96.9	327	9	US-09-925-664-47	Sequence 47, Appl
33	565	96.9	327	11	US-09-925-192-47	Sequence 47, Appl
34	565	96.9	327	13	US-10-047-542-26	Sequence 26, Appl
35	565	96.9	327	14	US-10-310-719-7	Sequence 7, Appl
36	565	96.9	327	14	US-10-112-582-4	Sequence 4, Appl
37	565	96.9	327	15	US-10-656-769-8	Sequence 8, Appl
38	565	96.9	327	17	US-10-822-300-114	Sequence 114, App
39	565	96.9	327	17	US-10-822-300-116	Sequence 116, App
40	565	96.9	327	17	US-10-872-932A-39	Sequence 39, Appl
41	565	96.9	327	17	US-10-891-972-171	Sequence 171, App
42	565	96.9	327	17	US-10-928-305-6	Sequence 6, Appl
43	565	96.9	327	17	US-10-891-658-6	Sequence 6, Appl
44	565	96.9	327	17	US-10-982-359-77	Sequence 77, Appl
45	565	96.9	327	17	US-10-937-596-30	Sequence 30, Appl

## ALIGNMENTS

RESULT 1  
US-10-959-318-9  
; Sequence 9, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 9  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)  
US-10-959-318-9

Query Match 98.8%; Score 576; DB 18; Length 110;  
Best Local Similarity 98.2%; Pred. No. 3.9e-48;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVFNWYVDGVEVHNATK 60  
Db 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVFNWYVDGVEVHNATK 60



Matches	108;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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Db	221	APEFAGSPSVLFP	PPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK	280					
Qy	61	PREEQFNSTYRVVSVLTVL	HQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	110					
Db	281	PREEQFNSTYRVVSVLTVL	HQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	330					
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US-09-968-362-20									
; Sequence 20, Application US/09968362									
; Publication No. US20030082679A1									
; GENERAL INFORMATION:									
; APPLICANT: Sun, Lee-Hwei K									
; APPLICANT: Sun, Bill									
; APPLICANT: Sun, Cecily R									
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor									
; FILE REFERENCE: 03SUN2001									
; CURRENT APPLICATION NUMBER: US/09/968,362									
; CURRENT FILING DATE: 2001-10-30									
; NUMBER OF SEQ ID NOS: 22									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 20									
; LENGTH: 449									
; TYPE: PRT									
; ORGANISM: Artificial Sequence									
; FEATURE:									
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2)									
; OTHER INFORMATION: B)									
US-09-968-362-20									
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Best Local Similarity 98.2%; Pred. No. 7.4e-47;									
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Db	233	APEFAGSPSVLFP	PPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK	292					
Qy	61	PREEQFNSTYRVVSVLTVL	HQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK	110					
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; Sequence 20, Application US/10800497									
; Publication No. US20040259209A1									
; GENERAL INFORMATION:									
; APPLICANT: Sun, Lee-Hwei K									
; APPLICANT: Sun, Bill									
; APPLICANT: Sun, Cecily R									
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-									
; TITLE OF INVENTION: stimulating factor with									
; TITLE OF INVENTION: increased biological activities									
; FILE REFERENCE: 03SUN2001									
; CURRENT APPLICATION NUMBER: US/10/800,497									
; CURRENT FILING DATE: 2004-03-15									
; PRIOR APPLICATION NUMBER: US/09/968,362									
; PRIOR FILING DATE: 2001-10-01									
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; FEATURE:									
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide									
; OTHER INFORMATION: (Figure 2)									

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; OTHER INFORMATION: B)
US-10-800-497-20

Query Match          97.8%; Score 570; DB 16; Length 449;
Best Local Similarity 98.2%; Pred. No. 7.4e-47;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 293 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 342

RESULT 10
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; Sequence 20, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2)
; OTHER INFORMATION: B)
US-10-800-449-20

Query Match          97.8%; Score 570; DB 16; Length 449;
Best Local Similarity 98.2%; Pred. No. 7.4e-47;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 233 APEFAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 292

QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 293 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 342

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US-10-006-593-67
; Sequence 67, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67
```

```
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67

Query Match          97.2%; Score 566.5; DB 14; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.7e-46;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 257 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315

QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 316 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 365

RESULT 12
US-10-307-724-67
; Sequence 67, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2cid
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 472
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-307-724-67

Query Match          97.2%; Score 566.5; DB 15; Length 472;
Best Local Similarity 99.1%; Pred. No. 1.7e-46;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 APPVAGGPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 257 APPVA-GPSVFLPPPKDGLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315

QY 61 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 316 PREEQFNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIISKAK 365

RESULT 13
US-10-737-290-67
; Sequence 67, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
```



; APPLICANT: Renshaw, Mark  
; APPLICANT: Orenchia, Cecilia  
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
; FILE REFERENCE: 1087-2 CIP III  
; CURRENT APPLICATION NUMBER: US/10/737,290  
; CURRENT FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: US 10/452,590  
; PRIOR FILING DATE: 2003-06-02  
; PRIOR APPLICATION NUMBER: US 10/307,724  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US 10/006,593  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/251,448  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/288,889  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/294,068  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 67  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized antibody heavy chain  
US-10-737-290-67

Query Match 97.2%; Score 566.5; DB 16; Length 472;  
Best Local Similarity 99.1%; Pred. No. 1.7e-46;  
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db 257 APPVA-GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315  
Qy 61 PREEQFNSTYRVVSVLTVLTQDNLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 316 PREEQFNSTYRVVSVLTVLTQDNLNGKEYCKVSNKGLPSSIEKTIKAK 365

RESULT 14  
US-10-959-318-4  
; Sequence 4, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; APPLICANT: Clark, Michael R  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-959-318-4

Query Match 96.9%; Score 565; DB 18; Length 110;  
Best Local Similarity 97.3%; Pred. No. 4.6e-47;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db 1 APEFLGGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Qy 61 PREEQFNSTYRVVSVLTVLTQDNLNGKEYCKVSNKGLPSSIEKTIKAK 110

Db 61 PREEQFNSTYRVVSVLTVLTQDNLNGKEYCKVSNKGLPSSIEKTIKAK 110  
RESULT 15  
US-11-018-102-24  
; Sequence 24, Application US/11018102  
; Publication No. US20050136061A1  
; GENERAL INFORMATION:  
; APPLICANT: Centocor, Inc.  
; TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN5045 USA NP  
; CURRENT APPLICATION NUMBER: US/11/018,102  
; CURRENT FILING DATE: 2004-12-21  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-018-102-24

Query Match 96.9%; Score 565; DB 20; Length 110;  
Best Local Similarity 97.3%; Pred. No. 4.6e-47;  
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db 1 APEFLGGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Qy 61 PREEQFNSTYRVVSVLTVLTQDNLNGKEYCKVSNKGLPSSIEKTIKAK 110  
Db 61 PREEQFNSTYRVVSVLTVLTQDNLNGKEYCKVSNKGLPSSIEKTIKAK 110

Search completed: November 17, 2005, 07:37:37  
Job time : 85.3836 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:11:49 ; Search time 89.9087 Seconds  
(without alignments)  
473.187 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583

Sequence: 1 APPVAGPSVFLPPPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1206590

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.9	110	2	AAR41717 Undefined
2	561	96.2	109	2	AAR67438 OKT3 mono
3	560	96.1	110	3	AAY54998 Mutated C
4	554.5	95.1	109	3	AAY54996 Mutated C
5	542.5	93.1	109	2	AAR41709 Undefined
6	542.5	93.1	109	3	AAY54997 Mutated C
7	541	92.8	110	2	AAR27680 Human imm
8	541	92.8	110	2	AAR41684 Undefined
9	541	92.8	110	8	ADH75385 Human IgG
10	538	92.3	102	8	ADJ52132 CH1 delet
11	537	92.1	109	7	ADD25659 Binding d
12	536	91.9	109	5	AAE28089 Human imm
13	536	91.9	110	8	ADH75415 CH2 regio
14	535	91.8	110	8	ADL90103 Human imm
15	534	91.6	110	8	ADH75413 CH2 regio
16	529	90.7	109	7	ADD25761 Binding d
17	525	90.1	105	2	AAY42626 Human IgG
18	525	90.1	110	2	AAR41713 Undefined
19	512	87.8	102	8	ADJ52129 CH1 delet
20	414	71.0	110	2	AAW71023 Mus muscu
21	399	68.4	110	1	AAP83207 Sequence
22	369	63.3	72	8	ADL15711 Human imm
23	328	56.3	66	2	AAR75349 C-gamma-1
24	328	56.3	66	2	AAR75351 C-gamma-1
25	327	56.1	76	8	ADL15713 Human imm

26	282	48.4	56	1	AAP83204	Aap83204 Sequence
27	277	47.5	56	1	AAP83201	Aap83201 Sequence
28	277	47.5	56	1	AAP83203	Aap83203 Sequence
29	276	47.3	56	1	AAP83202	Aap83202 Sequence
30	271	46.5	56	1	AAP83206	Aap83206 Sequence
31	271	46.5	56	1	AAP83205	Aap83205 Sequence
32	233	40.0	46	8	ADR59139	Adr59139 Human IgG
33	233	40.0	46	8	ADR59138	Adr59138 Human IgG
34	232.5	39.9	110	2	AAR33315	Aar33315 Variant I
35	227	38.9	46	8	ADR59143	Adr59143 Rhesus mo
36	225	38.6	46	8	ADR59142	Adr59142 Rhesus mo
37	206	35.3	46	8	ADR59140	Adr59140 Rhesus mo
38	206	35.3	46	8	ADR59141	Adr59141 Crab-eati
39	206	35.3	46	8	ADR59145	Adr59145 Pig IgG2a
40	206	35.3	46	8	ADR59148	Adr59148 Camel IgG
41	203	34.8	96	3	AA53640	Aab53640 Human col
42	201.5	34.6	110	2	AAR33316	Aar33316 Variant I
43	199	34.1	50	8	ADR59144	Adr59144 Optimum I
44	196	33.6	46	8	ADR59147	Adr59147 Llama IgG
45	196	33.6	46	8	ADR59152	Adr59152 Bovine Ig

ALIGNMENTS

RESULT 1  
AAR41717  
ID AAR41717 standard; protein; 110 AA.  
XX  
AC AAR41717;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-OCT-1993 (first entry)  
XX  
DE Undefined ORF2 encoded by plasmid pAH4808.  
XX

KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;  
KW light; chain; variable; constant; region; anti-human; pAH4807;  
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;  
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;  
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;  
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.  
XX  
OS Synthetic.  
XX  
PN WO9310819-A1.  
XX  
PD 10-JUN-1993.  
XX  
PF 24-NOV-1992; 92WO-US010206.  
XX  
PR 26-NOV-1991; 91US-00800458.  
XX  
PA (ALKE-) ALKERMES INC.  
XX  
PI Friden PM;  
XX  
DR WPI; 1993-196742/24.  
DR N-PSDB; AAQ43848.  
XX  
FT Antibody conjugates specific for transferrin receptor - used for  
FT diagnosis and treatment of cancer, AIDS and neurological disorders.  
XX  
PS Disclosure; Fig 19J; 151pp; English.  
XX

CC The sequences given in AAR41715-18 are encoded by the expression vector  
CC pAH4808. This vector represents the cloning of the human gamma isotype,  
CC gamma-4, with the variable region of the murine monoclonal antibody  
CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the  
CC heavy chain (VH) is derived from a murine source and the sequences  
CC encoding CH1, CH2 and CH3 are derived from a human source. This vector,  
CC in combination with the chimeric light chain vector, pAQ4611 (see also  
CC AAQ43845), was transfected into SP2/0 cells and clones were isolated.

CC 128.1 is an anti-human transferrin receptor antibody which binds to the  
 CC transferrin receptor on brain capillary endothelial cells. This antibody  
 CC may be used in a conjugate in which it is linked to a neuropharmaceutical  
 CC or diagnostic agent. The conjugate may be used to treat or prevent  
 CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
 CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
 CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 110 AA;

Query Match 96.9%; Score 565; DB 2; Length 110;  
 Best Local Similarity 97.3%; Pred. No. 4.9e-49;  
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLRPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60  
 DB 1 APEFLGGSPVFLRPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60  
 QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110

RESULT 2  
 AAR67438  
 ID AAR67438 standard; protein; 109 AA.  
 XX AAR67438;  
 AC  
 DT 25-MAR-2003 (revised)  
 DT 08-JUL-1995 (first entry)  
 XX  
 XX OKT3 monoclonal antibody fragment.  
 XX  
 KW OKT3; monoclonal antibody; antibody engineering; immunosuppressive;  
 KW humanized antibody.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9428027-A1.  
 XX  
 PD 08-DEC-1994.  
 XX  
 PF 01-JUN-1994; 94WO-US006198.  
 XX  
 PR 01-JUN-1993; 93US-00070116.  
 XX  
 PA (ARCH-) ARCH DEV CORP.  
 XX  
 PI Bluestone JA, Zivin RA, Jolliffe L;  
 XX  
 DR WPI; 1995-022721/03.  
 DR P-PSDB; AAQ75356.  
 XX

XX New humanised OKT3 antibody with mutated Fc receptor binding region -  
 PT useful as immunosuppressant to reduce transplant rejection, lacks the T-  
 PT cell activating side effects of wild type antibody.  
 XX  
 PS Disclosure; Page 82-87; 135pp; English.  
 XX

XX The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-  
 CC cell activating and immunosuppressive activity, and is used to treat  
 CC transplant patients to prevent rejection. The antibody can be engineered  
 CC to contain a human Fc region. By transferring the binding specificity  
 CC into a human framework, the immunogenicity is reduced without affecting  
 CC the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 109 AA;

Query Match 96.2%; Score 561; DB 2; Length 109;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-48;  
 Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPVAGGSPVFLRPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 61  
 DB 1 PEFLLGGSPVFLRPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 60  
 QY 62 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110  
 DB 61 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109

RESULT 3  
 AAY54998  
 ID AAY54998 standard; protein; 110 AA.  
 XX  
 AC AAY54998;  
 XX  
 DT 17-FEB-2000 (first entry)  
 XX

XX Mutated CH2 sequence G1deltaaac.  
 XX  
 DE  
 KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;  
 KW cell-mediated destruction; human; immunoglobulin G; Igg heavy chain;  
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
 KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;  
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;  
 KW sickle cell anaemia; coronary artery occlusion.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9558572-A1.  
 XX

PD 18-NOV-1999.  
 PF 07-MAY-1999; 99WO-GB001441.  
 PR 08-MAY-1998; 98GB-00009951.  
 XX  
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
 XX  
 PI Armour KL, Clark MR, Williamson LM;  
 XX  
 DR WPI; 2000-039075/03.  
 XX

PT Immunoglobulin-derived binding molecules that do not activate complement  
 PT or trigger cytotoxic activities and maintaining desirable immunoglobulin  
 PT properties.  
 XX  
 PS Claim 12; Fig 17; 81pp; English.  
 XX

XX This sequence represents the mutated CH2 molecule G1deltaaac, and is a  
 CC binding molecule of the invention. The recombinant binding molecule is  
 CC capable of binding a target molecule without triggering complement  
 CC dependent lysis, or the cell-mediated destruction of the target  
 CC comprises: (a) a binding domain capable of binding a target molecule; and  
 CC (b) an effector domain that is homologous to all or part of a constant  
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding  
 CC molecule is used to bind a target molecule (especially FcgammaRIIb  
 CC causing inhibition of B cell activation, mast cell degranulation or  
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the  
 CC binding of a second binding molecule, e.g. an antibody, to the target  
 CC molecule. The binding molecule is useful for the treatment of graft-vs-  
 CC host disease, organ transplant rejection, bone-marrow transplant  
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,  
 CC autoimmune thrombocytopenia and arthritis), alloimmunity (e.g.  
 CC foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),  
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN  
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and  
 CC coronary artery occlusion). The binding molecules do not activate  
 CC complement or trigger cytotoxic activities through FcgammaRIIb and desirable  
 CC IgG properties have been retained. The polypeptides do not contain non-



CC 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also CC AAQ43845), was transfected into sp2/0 cells and clones were isolated. CC 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody CC may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, CC Parkinsons and Alzheimers disease. It may also be used for diagnostic CC methods. (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 109 AA;  
Query Match 93.1%; Score 542.5; DB 2; Length 109;  
Best Local Similarity 93.6%; Pred. No. 8.9e-47;  
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 APPVAGSPSVFLFPKPKDLMISRTPEVTCVVVDVSDQEDPEVFQFNMYVDGVEVHNATK 60  
Db 1 APPVA-GPSVFLFPKPKDLMISRTPEVTCVVVDVSDQEDPEVFQFNMYVDGVEVHNATK 59  
Qy 61 PREQFNSTFRVSVLVTLVHODWLNQKEYKCKVSNKGLPDSIEKTIISKAK 110  
Db 60 PREQFNSTFRVSVLVTVHODWLNQKEYKCKVSNKGLPAPIEKTISKTK 109

RESULT 6  
AAV54997  
ID AAV54997 standard; protein; 109 AA.  
XX  
AC AAV54997;  
XX  
DT 17-FEB-2000 (first entry)  
XX  
DE Mutated CH2 sequence G2deltaa.  
XX  
KW Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;  
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;  
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;  
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;  
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;  
KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;  
KW autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis;  
KW neonatal autoimmune thrombocytopaenia; Goodpastures disease; therapy;  
KW sickle cell anaemia; coronary artery occlusion.  
XX  
OS Synthetic.  
OS  
PW WO9958572-A1.  
PN  
XX  
XX 18-NOV-1999.  
PD  
XX  
XX 07-MAY-1999; 99WO-GB001441.  
XX  
XX  
XX 08-MAY-1998; 98GB-00009951.  
PR  
XX  
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
PA  
XX  
XX Armour KL, Clark MR, Williamson LM;  
PI  
XX  
XX WPI; 2000-039075/03.  
DR  
XX  
XX Immunoglobulin-derived binding molecules that do not activate complement  
PT or trigger cytotoxic activities and maintaining desirable immunoglobulin  
PT properties.  
PT  
XX  
XX Claim 12; Fig 17; 81pp; English.  
PS  
XX  
XX This sequence represents the mutated CH2 molecule G2deltaa, and is a  
CC binding molecule of the invention. The recombinant binding molecule is  
CC capable of binding a target molecule without triggering complement  
CC

CC In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17.  
CC The inventor's propose eliminating these allotypes by amino acid changes  
CC to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype  
CC sites (1, 2 and 17) are located within the CH2 domain. New "isallotypes"  
CC should be suitable for therapeutic use in all patients. See AAR27678-  
CC R27681. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 110 AA; Query Match 92.8%; Score 541; DB 2; Length 110; Best Local Similarity 91.8%; Pred. No. 1.3e-46; Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy	<pre> 1 APPVAGGSPSVFLFPPKPKOTLIMISRTPEVTCTVVVDVSQEDPEVQFNWYVDGEVHNAKTK 60    :                                                                       </pre>
Db	<pre> 1 APELLGGSPSVFLFPPKPKOTLIMISRTPEVTCTVVVDVSIEDPEVKFNWYVDGEVHNAKTK 60 </pre>

Qy 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110

Db 61 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 110

RESULT 8  
AAR41684  
ID AAR41684 standard; protein; 110 AA.

	25-MAR-2003 (revised)	20-OCT-1993 (first entry)
DT		
DT		

DE Undefined ORF2 encoded by pAH4602.

Polymerase chain reaction; primer; PCR; amplify; murine, heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmacological; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.

OS Synthetic.

PN WO9310819-A1.

PD 10-JUN-1993.

PF 24-NOV-1992; 92WO-US010206.

PR 26-NOV-1991; 91US-00800458.

PA (ALKE-) ALKERMES INC.

PI Friden PM:

WPI: 1993-196742/24.

Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.

PS Disclosure: Fig 11K: 151pp: English.

The sequences given in AAR1682-95 are encoded by the expression vector, pAH4602. This vector contains open reading frames encoding the heavy chain variable region (VH) of the antibody 128.1, an ampicillin resistance gene and a histidine (histidinol) selection marker. Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into plasmid pAH44274. This was achieved by digesting the plasmid and the product with EcoRV and NheI. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin

CC receptor on brain capillary endothelial cells. This antibody may be used  
CC in a conjugate in which it is linked to a neuro- pharmaceutical or  
CC diagnostic agent. The conjugate may be used to treat or prevent  
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
CC methods. (Updated on 25-MAR-2003 to correct PN field.)

Query Match 92.8%; Score 541; DB 2; Length 110;  
Best Local Similarity 91.8%; Pred. No. 1.3e-45;  
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy	1 APPVAGGSPVFLFPDKPKDTLMISRTPVETCVVDVSQEDPEVQFNWYDGVVEVHNAKTK 60    :
Db	1 APELLGGSPVFLFPDKPKDTLMISRTPVETCVVDVSQEDPEVKFNWYDGVVEVHNAKTK 60    :

QY 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

61 PREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAK 110

RESULT 9  
ADH75385  
ID ADH75385 standard; protein; 110 AA.

22-APR-2004 (first entry)

Human IgG1 CH2 region.

AA Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
KW autoimmune disease; human; IgG; immunoglobulin.  
KW

OS Homo sapiens.

PN US2004002587-A1.

PD 01-JAN-2004.

20-FEB-2003; 2003US-00370749.

PR 20-FEB-2002: 2002US-0358161P.

PA (WATK/) WATKINS J D.

PI Watkins JD, Allan B;

DR WPI; 2004-070755/07.

New composition comprising a variant of a parent polypeptide having at least a portion of a Fe region, useful in treating e.g., autoimmune PT diseases.

PS Claim 20; SEQ ID NO 23; 62pp; English.

The invention relates to a new composition comprising a variant of a parent polypeptide having at least a portion of a FC region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the FC region. The composition is useful in treating diseases e.g., autoimmune diseases. The present sequence represents the amino acid sequence of a human immunoglobulin G<sub>1</sub> IgG<sub>1</sub> CH region.

Sequence 110 AA:

Query Match	92.8%;	Score 541;	DB 8;	Length 110;
Best Local Similarity	91.8%;	Pred. No. 1.3e-46;		
Matches 101;	Conservative	4;	Mismatches 5;	Indels 0;
				Gaps 0;





CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
 CC immunoglobulin hinge region polypeptide contains no more than one  
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
 CC capable of at least one immunological activity comprising antibody  
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
 CC binding domain polypeptide is capable of specifically binding to an  
 CC antigen. Also included are an isolated polynucleotide encoding the  
 CC binding domain-immunoglobulin fusion protein, a recombinant expression  
 CC construct comprising the polynucleotide (operably linked to a promoter),  
 CC a host cell transformed or transfected with a recombinant expression  
 CC construct, producing the binding domain-immunoglobulin fusion protein, a  
 CC pharmaceutical composition comprising the binding domain-immunoglobulin  
 CC fusion protein or polynucleotide and a carrier, and treating a subject  
 CC having or suspected of having a malignant condition or a B-cell disorder.  
 CC The binding domain-immunoglobulin fusion protein is useful for treating a  
 CC subject having or suspected of having a malignant condition or a B-cell  
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
 CC sclerosis or autoimmune disease. The present sequence is a binding domain  
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
 CC sequence data for this patent formed part of the printed specification  
 CC and is also available in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not  
 CC identified the sequences in the printed specification by their SEQ ID  
 CC number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 109 AA;

Query Match 92.1%; Score 537; DB 7; Length 109;  
 Best Local Similarity 91.7%; Pred. No. 3.2e-46;  
 Matches 100; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 PPVAGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNATKTP 61  
 DB 1 PELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTP 60  
 QY 62 REEQFNSTYRVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTISKAK 110  
 DB 61 REEQFNSTYRVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTISKAK 109

RESULT 12

AAE28089  
 ID AAE28089 standard; protein; 109 AA.

XX AAE28089;

XX 13-DEC-2002 (first entry)

XX Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.

XX Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;  
 XX vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;  
 XX immunosuppressive; lymphoid malignancy; respiratory syncytial virus;  
 XX anti-RSV; systemic infection; graft-versus-host disease; cytostatic;  
 XX virucide.

XX Homo sapiens.

XX WO200260919-A2.

XX 08-AUG-2002.

XX 12-DEC-2001; 2001WO-US048432.

XX 12-DEC-2000; 2000US-0254884P.

XX 09-MAY-2001; 2001US-0289760P.

XX (MEDI-) MEDIMMUNE INC.

XX Dall'acqua W, Johnson LS, Ward ES;

XX WPI; 2002-666925/71.

XX Modified immunoglobulins useful in the treatment of autoimmune diseases,  
 XX comprises at least one amino acid modification relative to a wild-type  
 XX immunoglobulin constant domain.

XX Disclosure; Page 138; 147pp; English.

XX The invention relates to a modified immunoglobulin (IgG1) which comprises  
 XX an IGH constant domain having at least one amino acid modification. The  
 XX immunoglobulins are used in the treatment or prevention of a disease or  
 XX disorder by passive immunotherapy for vaccinating a subject and for in  
 XX vivo diagnosis of a subject. The disease and disorders include a gamma  
 XX globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-  
 XX host, lymphoid malignancies and passive immunotherapies and also for the  
 XX treatment of various systemic infections. The present sequence is human  
 XX immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain

XX Sequence 109 AA;

Query Match 91.9%; Score 536; DB 5; Length 109;  
 Best Local Similarity 91.7%; Pred. No. 4e-46;  
 Matches 100; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNATKTK 60  
 DB 1 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTK 60

QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTISKAK 109

DB 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTISKAK 109

RESULT 13

ADH75415  
 ID ADH75415 standard; protein; 110 AA.

XX ADH75415;

XX 22-APR-2004 (first entry)

XX CH2 region K290S variant.

XX Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC;  
 XX autoimmune disease.

XX Unidentified.

XX US2004002587-A1.

XX 01-JAN-2004.

XX 20-FEB-2003; 2003US-00370749.

XX 20-FEB-2002; 2002US-0358161P.

XX (WATK/) WATKINS J D.

XX (ALLA/) ALLAN B.

XX Watkins JD, Allan B;

XX WPI; 2004-070755/07.

XX New composition comprising a variant of a parent polypeptide having at  
 XX least a portion of a Fe region, useful in treating e.g., autoimmune  
 XX diseases.

XX Disclosure; SEQ ID NO 53; 62pp; English.



Search completed: November 17, 2005, 07:47:01  
Job time : 90.9087 secs

11-17-05 11:27:14

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:37:49 ; Search time 16.5753 Seconds  
(without alignments)  
638.529 Million cell updates/sec

Title: US-09-674-857-12  
Perfect score: 583  
Sequence: 1 APPVAGSPVFLPPPKPDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 44790

Minimum DB seq length: 0  
Maximum DB seq length: 110

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278	47.7	88	2 A30503	Ig gamma-2b chain
2	140	24.0	107	2 I68730	IgE chain C3 regio
3	139	23.8	107	2 I68726	IgE chain C3 regio
4	133	22.8	106	1 K3HU	Ig kappa chain C r
5	132	22.6	110	2 S43147	Ig upsilon chain -
6	128.5	22.0	105	2 B26434	Ig lambda-5 chain
7	128	22.0	99	2 S26653	Ig kappa chain C r
8	128	22.0	103	2 B26167	Ig lambda chain C
9	127.5	21.9	105	2 B30554	Ig lambda chain C
10	122.5	21.0	106	2 S00259	Ig lambda-5 chain
11	120.5	20.7	105	1 L1MS	Ig lambda-1 chain
12	120.5	20.7	106	2 S22760	Ig lambda-2 chain
13	118	20.2	104	2 F53275	Ig kappa-1 chain C
14	117	20.1	99	2 A37927	Ig kappa chain C r
15	116	19.9	102	2 B34509	Ig light chain C r
16	114	19.6	103	1 K4RB	Ig kappa-B4 chain
17	109.5	18.8	105	1 L2HU	Ig lambda chain C
18	109.5	18.8	105	2 H32529	Ig lambda chain C
19	108.5	18.6	98	2 S26654	Ig lambda chain C
20	107	18.4	106	2 I50740	Ig lambda chain C
21	106	18.2	104	1 K5RBV	Ig kappa chain C r
22	106	18.2	106	2 I50741	Ig lambda chain -
23	105.5	18.1	109	1 L7RB	Ig lambda chain C
24	100	17.2	105	2 A27390	Ig lambda-1 chain
25	99.5	17.1	105	1 L1PG	Ig lambda chain C
26	99.5	17.1	106	1 K4RBS	Ig kappa-2 chain C
27	99.5	17.1	106	2 G20907	Ig kappa-B4 chain
28	99	17.0	106	1 K1MS	Ig kappa chain C r
29	94	16.1	103	1 K5RB	Ig kappa-B5 chain

30	94	16.1	105	2 B27390	Ig lambda-2 chain
31	92.5	15.9	102	2 I46731	lambda-chain C-reg
32	92.5	15.9	104	1 K9RB	Ig kappa-B9 chain
33	91	15.6	106	1 L1RTB	Ig kappa chain C r
34	90	15.4	104	1 L3MS	Ig lambda-3 chain
35	90	15.4	105	2 S22762	Ig lambda-2 chain
36	86	14.8	97	2 S26652	Ig gamma-1 chain C
37	86	14.8	106	1 K1RTA	Ig kappa chain C r
38	84.5	14.5	78	2 C34509	Ig light chain C r
39	80.5	13.8	78	2 D34509	Ig light chain C r
40	79	13.6	82	2 I57802	Ig lambda2-like ch
41	79	13.6	90	2 A24629	Ig gamma-3 chain C
42	76.5	13.1	67	2 PLO186	Ig lambda chain, C
43	76	13.0	104	1 L2MS	Ig lambda-2 chain
44	76	13.0	105	2 S22759	Ig lambda-2 chain
45	64.5	11.1	107	2 I68725	IgE chain C2 regio

ALIGNMENTS

RESULT 1

A30503  
Ig gamma-2b chain C region (ES.7A12) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C;Accession: A30503  
R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K.  
J. Immunol. 141, 1754-1761, 1988  
A;Title: DNA rearrangements affecting both variable and constant regions of Ig H chain  
A;Reference number: A30503; MUID:88315788; PMID:2842402  
A;Accession: A30503  
A;Molecule type: mRNA  
A;Residues: 1-88 <GIL>  
A;Cross-references: GB:M21925  
A;Experimental source: myeloma cell line MPC11  
A;Note: the authors translated the codon GAG for residue 41 as Ser  
C;Genetics:  
A;Introns: 46/3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-70/Domain: immunoglobulin homology <IMM>

Query Match 47.7%; Score 278; DB 2; Length 88;  
Best Local Similarity 63.2%; Pred. No. 6.6e-21;  
Matches 48; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY	24	SRTPEVTCVVVDVSQEDPEVQFNNVYDGVGVFNHAKTKPREEQNSTYRVVSVLTVLHQDW	83
DB	1	SLTPKVTCTVVVDVSEDDPDVQISFVNNVEVHTAQOTHRDYNSTIRVSVSTLPIQHODW	60
QY	84	LNKEYKCKVSNKGLP	99
DB	61	MSCKEFCCKVNNKDL	76

RESULT 2

I68730  
IgE chain C3 region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
C;Accession: I68730  
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.  
Immunogenetics 27, 288-292, 1988  
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s  
A;Reference number: I54443; MUID:88152907; PMID:3346043  
A;Accession: I68730  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-107 <RES>  
A;Cross-references: GB:M222933; NID:G194464; PIDN:AAA37915.1; PID:G194469  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;22-90/Domain: immunoglobulin homology <IMM>

```
Query Match      24.0%; Score 140; DB 2; Length 107;
Best Local Similarity 30.7%; Pred. No. 5.3e-07;
Matches 35; Conservative 22; Mismatches 31; Indels 26; Gaps 5;

Qy 7 GPSVFLPPPKDPTLMISRTPEVTCVVVDV-SQDPEVQFN-----WYVDGVEV 54
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 GVITYLPPSPFLD-LYQNGAPKLTCLVVDLSEKKNVNTWQEKKTGSASQWY---TKH 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 55 HNAKTKPREQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 HN-----NATTSITSLPVAKDWIEGYGQICVDHPDPKPIVRSITK 105
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
IGF chain C3 region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C:Accession: I68726
R:Shinkai, Y.; Nakauuchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A:Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s
A:Reference number: I54443; MUID:86152907; PMID:3346043
A:Accession: I68726
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-107 <RES>
A:Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:22-90/Domain: immunoglobulin homology <IMM>

Query Match      23.8%; Score 139; DB 2; Length 107;
Best Local Similarity 31.4%; Pred. No. 6.7e-07;
Matches 32; Conservative 20; Mismatches 48; Indels 2; Gaps 2;

Qy 7 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNNAKTKPREEQF 66
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 GVITYLPPSPFLD-LYQNGAPKLTCLVVDLSE-KNVNTWQEKKTGPSASQWYTKHHH 63
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 67 NSYRVSVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 NATTSITSLPVAKDWIEGYGQICVDHPDPKPIVRSITK 105
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
K3HU
IG kappa chain C region - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02
R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
Biochemistry 9, 3155-3161, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc
A:Reference number: A90562; MUID:71064023; PMID:5489770
A:Contents: myeloma protein Eu
A:Accession: B90562
A:Molecule type: protein
A:Residues: 1-106 <GOT>
A:Cross-references: UNIPROT:P01834
A:Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; Eu, disulfide bonds
R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ. Sub
A:Reference number: A91651; MUID:72188439; PMID:5027703
A:Contents: Bence Jones protein ri
A:Accession: A91651
A:Molecule type: protein
```

```
A:Residues: 1-106 <SUT>
R:Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Cell 22, 197-207, 1980
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
A:Reference number: A90806; MUID:81042304; PMID:6775818
A:Accession: A90806
A:Molecule type: DNA
A:Residues: 1-106 <HIE>
A:Cross-references: GB:J00241; NID:g331140; PIDN:CAA23823.1; PID:g1335148
A:Note: the sequence was determined from the germline gene
R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, I
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, I
A:Reference number: A94417
A:Contents: Bence Jones protein Roy
A:Accession: A94417
A:Molecule type: protein
A:Residues: 1-44, A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>
A:Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
R:Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A:Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A:Reference number: A91639; MUID:68242259; PMID:5586923
A:Contents: Bence Jones protein Cum
A:Accession: A91639
A:Molecule type: protein
A:Residues: 1-56, 'Q', 58-106 <HI2>
R:Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete i
A:Reference number: A92047; MUID:69234734; PMID:4893682
A:Contents: Bence Jones protein Ag
A:Accession: A92047
A:Molecule type: protein
A:Residues: 1-13, 'N', 15-106 <TIT>
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.
A:Reference number: A94242; MUID:70201507; PMID:5447531
A:Contents: Waldenstrom's macroglobulin Ou
A:Accession: A94242
A:Molecule type: protein
A:Residues: 1-13, 'N', 15-106 <KOH>
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A:Title: Km typing with PCR: application to population screening.
A:Reference number: A37927; MUID:91150772; PMID:1900145
A:Accession: B37927
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 8-106 <KUR>
A:Note: allotype Inv(3)
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances thei
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Genetics:
A:Gene: GDB:IGKC
A:Cross-references: GDB:120088; OMIM:147200
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into lai
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-86/Domain: immunoglobulin homology <IMM>
F:26-86/Disulfide bonds: #status experimental
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match      22.8%; Score 133; DB 1; Length 106;
Best Local Similarity 30.5%; Pred. No. 2.6e-06;
Matches 32; Conservative 26; Mismatches 41; Indels 6; Gaps 3;

Qy 8 PSVFLPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDG--EVHNAKTKPREEQ 65
```

```

Db 5 PSVFIFPP--PSDEQLKSGTASVCLNNFYPREAKVQ--WKVDNALQSGNSQESVTEQDS 60
Qy 66 FNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 61 KDSYVLSLSTLTSKADYKHKVYACEVTHQGLSSPVTKSNRGE 105

RESULT 5
S43147
Ig upsilon chain - duck (fragment)
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C:Accession: S43147
R:Mogor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
submitted to the EMBL Data Library, March 1994
A:Description: Evidence from duck immunoglobulin genes that Igy is the common ancestor
A:Reference number: S43145
A:Accession: S43147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <MAG>
A:Cross-references: EMBL:X78355; NID:G468612; PID:G468613
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 22.6%; Score 132; DB 2; Length 110;
Best Local Similarity 30.3%; Pred. No. 3.5e-06;
Matches 30; Conservative 20; Mismatches 47; Indels 2; Gaps 2;

Qy 10 VLFPPPKPDKTLMISRTPEVTCVVVDVSDPEVQFNNYVDGVEVHNKTKPREEQNST 69
Db 12 IFVFPSPG--GLYIRQDAKHCLVNL--PSDASISIGWREKSGALRDPMPVLTEHFNGT 69
Qy 70 YRVVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTSK 108
Db 70 FTASSLSAISQDWLAGERFCTVQHEDLPFLCKSIK 108

RESULT 6
B26434
Ig lambda-5 chain C region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C:Accession: B26434
R:Sakaguchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A:Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lympho
A:Reference number: A26434; MUID:87065143; PMID:3024017
A:Accession: B26434
A:Molecule type: mRNA
A:Residues: 1-105 <SAK>
A:Cross-references: GB:M30387
A:Note: the authors translated the codon TAC for residue 84 as Thr
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 22.0%; Score 128.5; DB 2; Length 105;
Best Local Similarity 34.3%; Pred. No. 7.3e-06;
Matches 36; Conservative 24; Mismatches 36; Indels 9; Gaps 6;

Qy 8 PSVFLPPPKDKTLMISRTPEVTCVVVDVSDPEVQFNNYVDGVEV--HNKTKPREEQ 65
Db 6 PLVTLFLPSLKN--LQPTR--POLVCL--VSEFYFGTLVDWVDGVPVTOGVETTPSKQ 60
Qy 66 FNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 61 TNNKIMVSSYTLISDQMPHRSYRCRVTHG--NTEKSVSPAE 103

RESULT 7
S26653
Ig kappa chain C region - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)

```

```

C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S26653
R:Enrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A:Reference number: S26652; MUID:91355693; PMID:2129418
A:Accession: S26653
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-99 <EHR>
A:Cross-references: EMBL:X65287
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 22.0%; Score 128; DB 2; Length 99;
Best Local Similarity 32.3%; Pred. No. 7.7e-06;
Matches 32; Conservative 22; Mismatches 39; Indels 6; Gaps 3;

Qy 8 PSVFLPPPKDKTLMISRTPEVTCVVVDVSDPEVQFNNYVDGVEV--HNKTKPREEQ 65
Db 5 PSVFIFPP--PSDEQLKSGTASVCLNNFYPREAKVQ--WKVDNALQSGNSQESVTEQDS 60
Qy 66 FNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEK 104
Db 61 KDSYVLSLSTLTSKADYKHKVYACEVTHQGLSSPVTK 99

RESULT 8
B26167
Ig lambda chain C region - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B26167
R:Parvari, R.; Ziv, E.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
A:Title: Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germi
A:Reference number: A26167; MUID:87218480; PMID:3107981
A:Accession: B26167
A:Molecule type: mRNA; DNA
A:Residues: 1-103 <PAR>
A:Cross-references: UNIPROT:P20763; GB:M33049
A:Note: 90-Asp was found in one cDNA clone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-87/Domain: immunoglobulin homology <IMM>

Query Match 22.0%; Score 128; DB 2; Length 103;
Best Local Similarity 30.3%; Pred. No. 8e-06;
Matches 33; Conservative 24; Mismatches 44; Indels 8; Gaps 5;

Qy 2 PPVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSDPEVQFNNYVDGVEVHNKTKP 61
Db 2 PKVA--PTTLFPSPS--KEELNEATKATLVCLINDFYPS--PVTVDWIDG--STRSGETTA 55
Qy 62 REEQFNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTSKAK 110
Db 56 PQRQNSQYMASSVLSASDSSSHETVTCRVTHG--TSITKTKERSE 102

RESULT 9
B30554
Ig lambda chain C region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30554
R:Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A:Reference number: A30554; MUID:89093962; PMID:2492052
A:Accession: B30554
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

```





## RESULT 13

F53275  
Ig kappa-1 chain C region b95 allotype - rabbit (fragment)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C/Accession: F53275  
R/Avadi, H.; Marche, P.N.; Cazenave, P.A.  
Immunogenetics 34, 201-207, 1991  
A/Title: Evolution of the rabbit immunoglobulin kappa chain genes.  
A/Reference number: A53275; MUID:91372868; PMID:1909995  
A/Accession: F53275  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-104 <A>  
A/Note: sequence inconsistent with nucleotide translation  
C/Species: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56170)  
C/Suprafamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;19-87/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 118; DB 2; Length 104;  
Best Local Similarity 29.1%; Pred. No. 8.1e-05;  
Matches 32; Conservative 26; Mismatches 38; Indels 14; Gaps 6;  
QY 3 PVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE-----VHNAK 58  
DB 2 PVA--PTVLFPSPSPAE--LATGTATTCV---ANKYFPDVTVMKVDGTTQTGTIENS 54  
QY 59 TKPREQFNSTYRVVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISK 108  
DB 55 TPQNSD--DCTYNLSSTLTLSKDEYNHSHDEYICQVA--QSGSPVVOQFSR 101

## RESULT 14

A37927  
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
C/Accession: A37927  
R/Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A/Title: Km typing with PCR: application to population screening.  
A/Reference number: A37927; MUID:91150772; PMID:1900145  
A/Accession: A37927  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-99 <KUR>  
C/Suprafamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;12-81/Domain: immunoglobulin homology <IMM>

Query Match 20.1%; Score 117; DB 2; Length 99;  
Best Local Similarity 28.4%; Pred. No. 9.6e-05;  
Matches 29; Conservative 26; Mismatches 41; Indels 6; Gaps 3;  
QY 11 FLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG--EVHNAKTKPREEQFNS 68  
DB 1 FIFP--PSDQLKSGTASVCLLNFFYPREAKVQ--WKVDNALQSGNSQESVTEQDSKDS 56  
QY 69 TYRVVSVLTVLHODWLNKGKCKVSNKGLPSSIEKTISKAK 110  
DB 57 TYSLSSTLTLSKADYKHKLYACEVTHQGLSSPVTKSFNRRGE 98

## RESULT 15

B34509  
Ig light chain C region 3 - sandbar shark (fragment)  
C/Species: Carcharhinus plumbeus (sandbar shark)  
C/Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 17-Nov-2000  
C/Accession: B34509  
R/Schluter, S.F.; Hohman, V.S.; Edmondson, A.B.; Marchalonis, J.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989  
A/Title: Evolution of immunoglobulin light chains: cDNA clones specifying sandbar shark

A/Reference number: A34509; MUID:90099382; PMID:2513577  
A/Accession: B34509  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-102 <SCH>  
A/Cross-references: GB:M29044; NID:g212941; PIDN:AAA49153.1; PID:g212942  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin

Query Match 19.9%; Score 116; DB 2; Length 102;  
Best Local Similarity 31.5%; Pred. No. 0.00013;  
Matches 29; Conservative 18; Mismatches 41; Indels 4; Gaps 3;  
QY 8 PSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG--VEVHNAKTKPREEQF 66  
DB 13 PSVSLPPSP--DQITAKNTATLCLVSGFKPGAAEIE--WTVDGSGVRGNGVETSRVQOEA 69  
QY 67 NSTYRVVSVLTVLHODWLNKGKCKVSNKGL 98  
DB 70 DNTFSVSSYLTLSASDNWSHELISCLVKHEAL 101

Search completed: November 17, 2005, 07:55:08  
Job time : 17.5753 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.8539 Seconds  
(without alignments)  
723.518 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 593

Sequence: 1 APPVAGGPSVFLPPPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.4

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	22.8	106	1	KAC_HUMAN
2	128	22.0	103	1	LAC_CHICK
3	122.5	21.0	105	1	LAC5_MUSSP
4	120.5	20.7	105	1	LAC1_MOUSE
5	119.5	20.5	105	1	LAC5_MOUSE
6	114	19.6	103	1	KAC4_RABIT
7	112.5	19.3	106	2	Q8TCU5
8	109.5	18.8	105	1	LAC_HUMAN
9	106	18.2	104	1	KAC6_RABIT
10	105.5	18.1	105	1	LAC_RABIT
11	100	17.2	104	1	LAC1_RAT
12	99.5	17.1	105	1	LAC_FIG
13	99.5	17.1	106	1	KACB_RABIT
14	99	17.0	106	1	KAC_MOUSE
15	94	16.1	103	1	KAC5_RABIT
16	94	16.1	104	1	LAC2_RAT
17	92.5	15.9	104	1	KAC9_RABIT
18	91	15.6	106	1	KACB_RAT
19	90	15.4	104	1	LAC3_MOUSE
20	86	14.8	106	1	KACA_RAT
21	76	13.0	104	1	LAC2_MOUSE
22	76	13.0	105	2	Q99JC1
23	71	12.2	107	2	Q8KY10
24	71	12.2	107	2	Q6EZ15
25	62.5	10.7	74	2	P79659
26	62.5	10.7	74	2	P79659
27	62	10.6	79	1	SNSP_HUMAN
28	62	10.6	93	2	O6LB79
29	61.5	10.5	93	2	O6LBW2
30	61	10.5	98	2	Q7XZF9
31	59	10.1	73	2	Q8FBY4

32	59	10.1	93	2	Q31158
33	58.5	10.0	93	2	O19471
34	58.5	10.0	93	2	O19472
35	58.5	10.0	93	2	Q6GVI4
36	58.5	10.0	93	2	Q9QUH8
37	58	9.9	90	1	ALB2_SULTO
38	58	9.9	91	2	Q9JKF1
39	58	9.9	110	2	O66084
40	57.5	9.9	74	2	P79661
41	57.5	9.9	95	1	DAFT_TRYCR
42	57	9.8	91	2	Q31248
43	57	9.8	106	2	Q31261
44	56.5	9.7	104	2	Q30837
45	56	9.6	63	2	Q6EHZ1

## ALIGNMENTS

RESULT 1

KAC\_HUMAN

ID KAC\_HUMAN STANDARD; PRT; 106 AA.

AC P01834;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ig kappa chain C region.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE (MYELOMA PROTEIN EU).

RX MEDLINE=71064023; PubMed=5489770;

RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";

RL Biochemistry 9:3155-3161(1970).

RN [2]

RP DISULFIDE BONDS.

RX MEDLINE=71064027; PubMed=4923144;

RA Gall W.E., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";

RL Biochemistry 9:3188-3196(1970).

RN [3]

RP SEQUENCE (BENCE-JONES PROTEIN TI).

RX MEDLINE=72188439; PubMed=5027703;

RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";

RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;

RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;

RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";

RL Cell 22:197-207(1980).

RN [5]

RP SEQUENCE (BENCE-JONES PROTEIN ROY).

RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;

RL (in) Franek F., Shugar D. (eds.);

RL Gamma Globulins: structure and function, pp.57-74, Academic Press, New York (1969).

RN [6]

RP SEQUENCE (BENCE-JONES PROTEIN CUM).

RX MEDLINE=68242259; PubMed=5586923;

RA Hilschmann N.;

Q31158	mus musculus
O19471	mus musculus
O19472	mus musculus
Q6GVI4	bos taurus
Q9QUH8	mus musculus
Q971T6	sulfolobus
Q9JKF1	marmota mon
O66084	lactococcus
P79661	oncorhynch
Q36327	trypanosoma
Q31248	peromyscus
Q31261	tattus norv
Q30837	ovis aries
Q6EHZ1	homo sapien



Query Match 22.0%; Score 128; DB 1; Length 103;  
Best Local Similarity 30.3%; Pred. No. 5.1e-05;  
Matches 33; Conservative 24; Mismatches 44; Indels 8; Gaps 5;

QY 2 PVVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKP 61  
DB 2 PKVA--PFTTLFPPS-KEELNEATKATLVCLINDFPYS--PVTVDWIDG-STRSGETTA 55  
QY 62 REQFNSTYRVSVLTVLHQDLNGKEYKCKVSKNGLPSSIEKTIKAK 110  
DB 56 PQRSQNSQYMASSYLSASDSSSHETVTCRVTHG--TSITKTKRSE 102

## RESULT 3

LACS MUSSP STANDARD; PRT; 105 AA.  
AC P20765;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda-5 chain C region.  
OS Mus spretus (western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88196070; PubMed=3129289;  
RA Mami F., Cazenave P.A., Kindt T.J.,  
RT "Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";  
RL EMBL J. 7:117-122(1988).  
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -----  
DR EMBL; M35582; AAA39152.1; -;  
DR HSSP; P01843; IJNH.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig CL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00407; IGC1; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON TER 1 100 Ig-like.  
FT DOMAIN 6 100  
FT DISULFID 27 86  
FT INTERPRO; IPR007110; Ig-like.  
FT DISULFID 104 104 Interchain (with heavy chain).  
SQ SEQUENCE 105 AA; 11674 MW; AAB417DF68471A17 CRC64;

Query Match 21.0%; Score 122.5; DB 1; Length 105;  
Best Local Similarity 33.3%; Pred. No. 0.00019;  
Matches 35; Conservative 23; Mismatches 38; Indels 9; Gaps 5;

QY 8 PSVLFPPKPKDTLMISRTPEVTCVVVDVSDQEDP-EVQFNWYVDGVEV-HNAKTKPREQ 65  
DB 6 PLVTLFPLSKNL-----QANKVLVCL-VSEFYPTLVDMKVDGVPVQTGVETTPQSKQ 60  
QY 66 FNSTYRVSVLTVLHQDLNGKEYKCKVSKNGLPSSIEKTIKAK 110  
DB 61 TNNKYMVSSYLTLLISDQMPHSRYSCRVTHEG--NTVEKSVSPAE 103

## RESULT 4

LACS\_MOUSE STANDARD; PRT; 105 AA.  
AC P01843;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ig lambda-1 chain C region.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83014953; PubMed=6812053;  
RA Selsing E., Miller J., Wilson R., Storb U.,  
RT "Evolution of mouse immunoglobulin lambda genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).  
[2]  
RP SEQUENCE FROM N.A. (MOPC 315).  
RX MEDLINE=81148806; PubMed=6259534;  
RA Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,  
RA Gelfand M.L., Baltimore D.,  
RT "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";  
RL Nature 230:65-67(1981).  
[3]  
RP SEQUENCE FROM N.A. (S43).  
RX MEDLINE=82220143; PubMed=6283385;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.,  
RT "Somatic variants of murine immunoglobulin lambda light chains.";  
RL Nature 298:380-382(1982).  
[4]  
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).  
RX MEDLINE=71107854; PubMed=5276767;  
RA Appella E.,  
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).  
CC -|- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1  
CC normal lambda-2 chain and 1 abnormal lambda-1 chain that is  
CC missing a large part of the V region. The C region sequence (shown  
CC here) appears completely normal.  
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00582; AAA51636.1; -;  
DR EMBL; J00587; AAB59672.1; -;  
DR PIR; A93922; LIMS.  
DR PDB; 1JNH; X-ray; A=1-105  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW 3D-structure: Direct protein sequencing; Immunoglobulin C region;  
KW Immunoglobulin domain.  
FT NON TER 1 100 Ig-like.  
FT DOMAIN 6 100  
FT DISULFID 27 86 Interchain (with heavy chain).  
FT DISULFID 104 104 ET -> TE (in Ref. 4).  
FT CONFLICT 19 20 Q -> E (in Ref. 4).  
FT CONFLICT 56 56 Missing (in Ref. 4).  
FT CONFLICT 75 75 HS -> SH (in Ref. 4).  
FT CONFLICT 81 82 S -> SS (in Ref. 4).  
FT CONFLICT 85 85 E -> Q (in Ref. 4).  
FT CONFLICT 96 96  
FT STRAND 4 4  
FT STRAND 7 7

```
FT STRAND 10 11
FT HELIX 15 19
FT TURN 20 21
FT STRAND 22 33
FT STRAND 37 43
FT TURN 44 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 52 54
FT STRAND 58 60
FT TURN 61 63
FT STRAND 64 74
FT HELIX 75 80
FT STRAND 84 90
FT TURN 91 92
FT STRAND 93 99
SQ SEQUENCE 105 AA; 11575 MW; A89F2B09BCFCA018 CRC64;

Query Match 20.7%; Score 120.5; DB 1; Length 105;
Best Local Similarity 30.1%; Pred. No. 0.0003;
Matches 31; Conservative 21; Mismatches 44; Indels 7; Gaps 4;

QY 8 PSVFLPPPKDILMISRTPEVTCVVVDVSQEDPDEVFQFNWYDGVGV-HNAKTKPREQF 66
DB 6 PSVTLFPPSSEE--LETNKAATLVCTITDF--YFGVWTVDMKVDGTPVTQGMETTPSPKQS 61
QY 67 NSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTSKA 109
DB 62 NNKYMASSYLTLTARAWERHSSCQVTHGEG--HTVEKSLSRA 102

RESULT 5
LACS MOUSE
ID _LACS_MOUSE STANDARD; PRT; 105 AA.
AC P20764;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-5 chain C region.
GN Name=Igl-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87065143; PubMed=3024017;
RA Sakaguchi N., Melchers F.;
RT "Lambda 5, a new light-chain-related locus selectively expressed in
RT pre-B lymphocytes."
RL Nature 324:579-582(1986).
CC -!- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----
CC EMBL; M30387; ; NOT_ANNOTATED_CDS.
CC DR HSSP; P01843; 1JNH.
CC MGD; MGI:96529; Igl-5.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC SMART; SM00407; IGC1; 1_
CC PROSITE; PSS0835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
```

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FT DOMAIN 6 100
FT DISULFID 27 86
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11678 MW; 1F210915904A86A5 CRC64;

Query Match 20.5%; Score 119.5; DB 1; Length 105;
Best Local Similarity 33.3%; Pred. No. 0.00037;
Matches 35; Conservative 24; Mismatches 37; Indels 9; Gaps 6;

QY 8 PSVFLPPPKDILMISRTPEVTCVVVDVSQEDP-EEVQFNWYDGVGV-HNAKTKPREQ 65
DB 6 PLVTLEFLPSLKN-LQPTR-PQLVCL---VSEFYPTGLVDMKVDGVPVQTQVETTPSPKQ 60
QY 66 FNSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTSKAK 110
DB 61 TNKNYVSSYLTLISDQWMPHSRTSCRTHGEG--NTVEKSVSPAE 103

RESULT 6
KAC4 RABBIT
ID _KAC4_RABBIT STANDARD; PRT; 103 AA.
AC P01840;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa-b4 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83300036; PubMed=6412231;
RA Emorine L., Dreher K.D., Kindt T.J., Max E.E.;
RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
RT allotype J-C locus and evidence for several b4-related sequences in
RT the rabbit genome."
RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82060334; PubMed=6795636;
RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT "Nucleotide sequence of constant and 3' untranslated regions of a
RT kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit."
RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
RN [3]
RP SEQUENCE.
RX MEDLINE=75133568; PubMed=1091650;
RA Chen K.C.S., Kindt T.J., Krause R.M.;
RT "Primary structure of the L chain from a rabbit homogeneous antibody
RT to streptococcal carbohydrate. II. Sequence determination of peptides
RT from tryptic and peptic digests."
RL J. Biol. Chem. 250:3289-3296(1975).
CC -!- MISCELLANEOUS: This chain was obtained from antibody to the
CC specific carbohydrate of group C Streptococci and was isolated
CC from the serum of a single rabbit
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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-----
CC EMBL; X00231; CAA25051.1; -.
CC PIR; A93971; K4RB.
CC DR HSSP; P01837; 1KCV.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Igi; 1.
CC PROSITE; PSS0835; IG_LIKE; 1.
```

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DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 5 95 Ig-like.
FT DISULFID 26 85
FT DISULFID 103 103 Interchain (with a heavy chain).
FT CONFLICT 58 58 N -> D (in Ref. 3).
SQ SEQUENCE 103 AA; 11043 MW; 5FC5ACC8B60B68DB CRC64;

Query Match 19.6%; Score 114; DB 1; Length 103;
Best Local Similarity 31.4%; Pred. No. 0.0013;
Matches 33; Conservative 20; Mismatches 38; Indels 14; Gaps 6;

Qy 3 PVAGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE----VHNAK 58
Db 2 PVA--PTVLIPPAADQ--VATGRTIVCV---ANKYFPDVTVTWEVDGTTQTGTGIESK 54
Qy 59 TKPREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE 103
Db 55 TP--QNSADCTYNLSSTLTSTQYNSHKYETCKVT-QGTTSSVQ 96

RESULT 7
Q8TCJ5 PRELIMINARY; PRT; 106 AA.
AC Q8TCJ5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp667J0810 (Fragment).
GN Name=DKFZp667J0810;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (Sep-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR HSSP; P01842; ILIL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 19.3%; Score 112.5; DB 2; Length 106;
Best Local Similarity 28.7%; Pred. No. 0.0019;
Matches 29; Conservative 22; Mismatches 43; Indels 7; Gaps 4;

Qy 8 PSVLFPPPKDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEYH-NAKTKPREQF 66
Db 7 PSVTLFPPSSEE--LQANKATLVCLISDF--YPGAVTVAMKADSSPVKAGVETTTPSKQS 62
Qy 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIS 107
Db 63 NNKYAASSYLSLTPEQWQSHKSKSCQVTHEG--STVEKTV 101

RESULT 8
LAC_HUMAN
ID --LAC_HUMAN
AC P01842; P80423;
PRT; 105 AA.
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda chain C regions.
GN Name=IGLC1;
GN and
GN Name=IGLC2;
GN and
GN Name=IGLC3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE (BENCE-JONES PROTEIN SH).
MEDLINE=70156723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein. 3. The
complete amino acid sequence and the location of the disulfide
bridges."
J. Biol. Chem. 245:2171-2176(1970).

[2]
SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
MEDLINE=69088380; PubMed=4883641;
Milstein C., Clegg J.B., Jarvis J.M.;
"Immunoglobulin lambda-chains. The complete amino acid sequence of a
Bence-Jones protein."
Biochem. J. 110:631-652(1968).

[3]
SEQUENCE (BENCE-JONES PROTEIN NIG-64).
MEDLINE=83186114; PubMed=6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
"Comparative studies on the structure of the light chains of human
immunoglobulins. IV. Assignment of a subgroup."
J. Biochem. 93:421-429(1983).

[4]
SEQUENCE (BENCE-JONES PROTEIN KERN).
MEDLINE=71150336; PubMed=5549568;
Ponstingl H., Hees M., Hilschmann N.;
"Structural rule of antibodies. Primary structure of a monoclonal
immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
protein Kern). V. The complete amino acid sequence and its genetic
interpretation."
Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).

[5]
PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
MEDLINE=74109253; PubMed=4814727;
Chen B.L., Poljak R.J.;
"Amino acid sequence of the (lambda) light chain of a human myeloma
immunoglobulin (IG New)."
Biochemistry 13:1295-1302(1974).

[6]
SEQUENCE (DOT).
MEDLINE=95252598; PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
"Characterization of the two unique human anti-flavin monoclonal
immunoglobulins."
Eur. J. Biochem. 228:886-893(1995).

[7]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
MEDLINE=75046825; PubMed=4215080;
Poljak R.J., Anzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
Saul P.;
"The three-dimensional structure of the fab' fragment of a human
myeloma immunoglobulin at 2.0-A resolution."
Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).

[8]
PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
MEDLINE=75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
"Primary structure of the MCG lambda chain."
Biochemistry 13:4102-4114(1974).
```





```
-----NOT_ANNOTATED_CDS.
CC EMBL; X00032; -, NOT_ANNOTATED_CDS.
DR EMBL; K01363; AAA31355.1; -.
DR PIR; A02124; KSRBV.
DR HSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 5 100 Ig-like.
FT DISULFID 26 85
FT DISULFID 104 104 Interchain (with a heavy chain).
FT CONFLICT 1
FT CONFLICT 104 AA; 11079 MW; 7C71850205381751 CRC64;
SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 18.2%; Score 106; DB 1; Length 104;
Best Local Similarity 26.7%; Pred. No. 0.0082;
Matches 28; Conservative 25; Mismatches 40; Indels 12; Gaps 5;

QY 8 PSVLFPPPKKDTLMISRTVEVTCVVVDVSDQEDPEVFQFNWYVDG-----VEVHNATKPRE 63
DB 5 PTVLFFPPSPAE--LATGTATVVCV---ANKYFPDGTVTWQDVGKPLTTGTIETSKTPQNS 59
QY 64 EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 108
DB 60 D-DCTNLSTLTLSKDEYNHDEYTCQVA-QSGSPVQVSFSR 101

RESULT 10
LAC_RABIT
ID LAC_RABIT STANDARD; PRT; 105 AA.
AC P01847;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=82091105; PubMed=6797414;
RA Garcia I., Jaton J.-C.;
RT "The primary structure of the constant region of Basilea-rabbit
immunoglobulin lambda-chains.";
RL Biochem. J. 197;177-183(1981).
CC -1- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
specificity.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02130; L7RB.
DR HSP; P01842; IAQK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Direct protein sequencing; Immunoglobulin C region;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 100 Ig-like.
FT DISULFID 27 86
FT DISULFID 104 104 Interchain (with heavy chain).
FT SEQUENCE 105 AA; 11484 MW; B42751327288663D CRC64;

Query Match 18.1%; Score 105.5; DB 1; Length 105;

us-09-674-857-12.LL.rup
Best Local Similarity 26.9%; Pred. No. 0.0093;
Matches 28; Conservative 22; Mismatches 47; Indels 7; Gaps 4;

QY 8 PSVLFPPPKKDTLMISRTVEVTCVVVDVSDQEDPEVFQFNWYVDGVEV-HNAKTKPREQF 66
DB 6 PSVILFPPSSEE--LKDKNKATLVCLISDFYPR--TVKVNWKADGNSVTQGVDTTQPSKQS 61
QY 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 62 NNKYAASSFLHLTANQWKYSQSVTCQVTHEG--HTVEKSLAPAE 103

RESULT 11
LAC1_RAT
ID LAC1_RAT STANDARD; PRT; 104 AA.
AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes
and a single V lambda gene.";
RL Gene 55;75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; M22520; AAA41419.1; ALT_INIT.
DR HSP; P01843; LUNH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN 6 99 Ig-like.
FT DISULFID 27 85
FT DISULFID 103 103 Interchain (with heavy chain).
SQ SEQUENCE 104 AA; 11565 MW; CBF71811F4BC878A CRC64;

Query Match 17.2%; Score 100; DB 1; Length 104;
Best Local Similarity 27.4%; Pred. No. 0.033;
Matches 29; Conservative 22; Mismatches 43; Indels 12; Gaps 5;

QY 8 PSVLFPPPKKDTLMISRTVEVTCVVVDVSDQEDPEVQ-FNMYVDGVEVHNATKPREE 64
DB 6 PSVTLFPPSSEEL---KTDKATLVCMVTDYF---PGVMVVMWKADGTPITQGVETTQPF 58
QY 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 59 KQNNKYMATSYLLLTAKAWETHSNYSQVTHE--ENTVEKSLRAE 102

RESULT 12
LAC_PIG
ID LAC_PIG STANDARD; PRT; 105 AA.
```



FT	TURN	60	62
FT	STRAND	65	74
FT	HELIX	75	79
FT	TURN	80	80
FT	STRAND	83	89
FT	TURN	91	92
FT	STRAND	97	102
FT	TURN	103	106
SQ	SEQUENCE	106 AA; 4B51FF5EF49BAEB5 CRC64;	
 Query Match 17.0%; Score 99; DB 1; Length 106; Best Local Similarity 25.2%; Pred.No. 0.042; Matches 26; Conservative 23; Mismatches 48; Indels 6; Gaps 3;			
Qy	8 PSYFLPPPKDLMISRTPEVTCVVVDVSQEDPEVFQFNMYVDGVFHNA--KTKPREEQ 65	: ::   :	-LTSGGASVVCFLNNFVKD--INVKKIDGSRQNGVLNSWTDQDS 60
Dd	5 PTYSIFPSSSEQ--LTSGGASVVCFLNNFVKD--INVKKIDGSRQNGVLNSWTDQDS 60	:	:
Qy	66 PSTYRVSVSLTVLHODWLNGKEYCKVKSNKGLPSSIETKISK 108	::   :	::   :
Dd	61 KDSTYSMSSTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNR 103	:	:
 RESULT 15			
KACS_RABIT	STANDARD;	PRT;	103 AA.
ID - KACS_RABIT	AC P01841;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DT	Ig kappa-b5 chain C region.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=E83178897; PubMed=6404296;		
RA	Avadi H., Dutka S., Paroutaud P., Strosberg A.D.;		
RA	"Partial amino acid sequence of a rabbit immunoglobulin light chain of		
RT	allotype b5";		
RL	Biochemistry 22:993-998(1983).		
RL	[2]		
RP	SEQUENCE OF 4-103.		
RP	MEDLINE=E2057807; PubMed=6795448; DOI=10.1016/0161-5890(80)90177-7;		
RA	Chersi A., Alexander C.B., Mage R.G.;		
RA	"Partial primary structure of the immunoglobulin light chain constant		
RT	region of a single rabbit of b5 allotype.";		
RL	Mol. Immunol. 17:1515-1523(1980).		
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.		
DR	PIR; A90480; KSRB.		
DR	HSP; P01837; LKCU.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003597; Ig_c1.		
DR	InterPro; IPR003066; Ig_MHC.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00407; IGc1; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
DR	PROSITE; PS00290; IG_MHC; FALSE_NEG.		
KW	Direct protein sequencing; Immunoglobulin C region;		
KW	Immunoglobulin domain.		
FT	NON TER 1 1		
FT	DOMAIN 5 99		Ig-like.
FT	DISULFID 26 85		
FT	DISULFID 103 103		Interchain (with a heavy chain).
FT	CONFLICT 5 5		Missing (in Ref. 2).
FT	CONFLICT 14 14		P -> S (in Ref. 2).
FT	CONFLICT 21 21		A -> T (in Ref. 2).
FT	CONFLICT 82 82		E -> Q (in Ref. 2).
FT	CONFLICT 87 88		VA -> LP (in Ref. 2).
SQ	SEQUENCE 103 AA; 10945 MW; F33800791B031DD3 CRC64;		
 Query Match 16.1%; Score 94; DB 1; Length 103;			



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:32:09 ; Search time 23.6073 Seconds  
(without alignments)  
347.833 Million cell updates/sec

Title: US-09-674-857-12

Perfect score: 583

Sequence: 1 APPVAGPSVFLPPPKPKDT.....CKVSNKGLPSSIBKTSKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 333962

Minimum DB seq length: 0

Maximum DB seq length: 110

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*

5: /cgn2\_6/ptodata/1/iaa/PTUTS COMB.pcp.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	565	96.9	110	3	US-08-444-644-44
2	565	96.9	110	3	US-08-232-246A-44
3	561	96.2	109	2	US-08-070-116A-4
4	561	96.2	109	4	US-08-557-050-4
5	542.5	93.1	109	3	US-08-444-644-30
6	542.5	93.1	109	3	US-08-232-246A-30
7	541	92.8	110	3	US-08-444-644-21
8	541	92.8	110	3	US-08-232-246A-21
9	525	90.1	105	2	US-08-232-539D-60
10	525	90.1	110	3	US-08-444-644-38
11	525	90.1	110	3	US-08-232-246A-38
12	528	56.3	66	3	US-08-569-147-85
13	179	30.7	107	4	US-09-281-760B-36
14	166.5	28.6	106	2	US-08-232-539D-54
15	152	26.1	109	3	US-08-466-163B-1
16	152	26.1	109	4	US-09-802-096-1
17	152	26.1	109	4	US-09-802-077-1
18	142	24.4	100	1	US-08-422-101-10
19	142	24.4	100	1	US-08-422-091-10
20	142	24.4	100	2	US-08-422-092-10
21	142	24.4	100	2	US-08-788-800-7
22	142	24.4	100	3	US-08-422-093-10
23	142	24.4	100	3	US-08-422-112-10
24	133	22.8	105	3	US-09-025-769B-166
25	133	22.8	105	4	US-09-490-070A-166
26	133	22.8	105	4	US-09-490-153-166
27	133	22.8	105	4	US-09-490-324-166

28 133 22.8 106 2 US-08-378-939-40 Sequence 40, Appl  
29 133 22.8 106 2 US-08-761-277A-49 Sequence 49, Appl  
30 133 22.8 106 3 US-08-444-644-26 Sequence 26, Appl  
31 133 22.8 106 3 US-08-232-246A-26 Sequence 26, Appl  
32 133 22.8 107 1 US-08-422-101-8 Sequence 8, Appl  
33 133 22.8 107 1 US-08-422-091-8 Sequence 8, Appl  
34 133 22.8 107 2 US-08-422-092-8 Sequence 8, Appl  
35 133 22.8 107 2 US-08-788-800-5 Sequence 5, Appl  
36 133 22.8 107 3 US-08-422-093-8 Sequence 8, Appl  
37 133 22.8 107 3 US-08-422-112-8 Sequence 8, Appl  
38 133 22.8 107 4 US-09-301-593-20 Sequence 20, Appl  
39 133 22.8 108 4 US-09-313-942-13 Sequence 13, Appl  
40 129 22.1 106 1 US-08-399-106A-7 Sequence 7, Appl  
41 129 22.1 106 1 US-08-433-105A-7 Sequence 7, Appl  
42 129 22.1 106 2 US-08-434-869A-7 Sequence 7, Appl  
43 127.5 21.9 109 2 US-08-646-981-6 Sequence 6, Appl  
44 127 21.8 109 1 US-08-436-463-8 Sequence 8, Appl  
45 127 21.8 109 1 US-08-024-253-8 Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-08-444-644-44  
; Sequence 44, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Fiden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-8240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-44

Query Match      96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
Db 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110

RESULT 2
US-08-232-246A-44
; Sequence 44, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Fiden, Phillip M.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-44

Query Match      96.9%; Score 565; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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Db 1 APEFLGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
Db 61 PREQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110

RESULT 3
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: Of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-070-116A-4

Query Match      96.2%; Score 561; DB 2; Length 109;
Best Local Similarity 97.2%; Pred. No. 4e-60;
Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEVAGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
Db 1 PEFLGGPSVFLPPPKDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 60

QY 62 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
Db 61 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 109

RESULT 4
US-08-557-050-4
; Sequence 4, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
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; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-050-4

Query Match 96.2%; Score 561; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 4e-60; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 3;

Qy 2 PVVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKP 61
Db 1 PFLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKP 60

Qy 62 REQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110
Db 61 REQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 109

RESULT 5
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-30

Query Match 93.1%; Score 542.5; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-58;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTK 59

Qy 61 PREQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAK 110
Db 60 PREQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAK 109

RESULT 6
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-232-246A-30

Query Match 93.1%; Score 542.5; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-58;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APPVA-GPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 59

QY 61 PREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 60 PREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKGLPAPIETIKTK 109

RESULT 7
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA: PCT/US90/05077
; FILING DATE: 07-SEP-1990
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-444-644-21

Query Match 92.8%; Score 541; DB 3; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.1e-57;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APPELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

QY 61 PREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAK 110
Db 61 PREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKGLPAPIETIKAK 110

RESULT 8
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329506
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
```



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; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-232-246A-21

Query Match          92.8%; Score 541; DB 3; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.1e-57;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVHNAKTK 60

Qy 61 PREEQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
Db 61 PREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110

RESULT 9
US-08-232-539D-60
; Sequence 60, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IgE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-232-539D-60

Query Match          90.1%; Score 525; DB 2; Length 105;
Best Local Similarity 94.2%; Pred. No. 8.6e-56;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 GPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQF 66
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Db 1 GPSVFLPPKPKDTLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVHNAKTKPREEQY 60
Qy 67 NSTYRVSVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
Db 61 NSTYRVSVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 104

RESULT 10
US-08-444-644-38
; Sequence 38, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-444-644-38

Query Match          90.1%; Score 525; DB 3; Length 110;
Best Local Similarity 90.0%; Pred. No. 9.2e-56;
Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 APPVAGSPSVLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTK 60
Db 1 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVHNAKTK 60

Qy 61 PREEQFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTSKAK 110
Db 61 LREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTISKAK 110
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RESULT 11
US-08-232-246A-38
; Sequence 38, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTI-BODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-38

Query Match 90.1%; Score 525; DB 3; Length 110;
Best Local Similarity 90.0%; Pred. No. 9.2e-56;
Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNATK 60
Db 1 APELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNATK 60
Qy 61 PREQFNSTYRVVSVLTVTLQHDWLNQKEYKCKVSNKGLPSSIEKTIKAK 110
Db 61 LREEQNSTFRVSVLTVTLQHDWLNQKEYKCKVSNKALPAPIETIKAK 110

RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
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; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-85

Query Match 56.3%; Score 328; DB 3; Length 66;
Best Local Similarity 90.9%; Pred. No. 3.1e-32;
Matches 60; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNATK 60
Db 1 APELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNATK 60
Qy 61 PREEQF 66
Db 61 PREEQY 66

RESULT 13
US-09-281-760E-36
; Sequence 36, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)-(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (413)..(414) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (451)..(451) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (460)..(462) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (500)..(500) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (530)..(530) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (568)..(568) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (847)..(849) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (853)..(853) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1382)..(1382) stands for any nucleic acid  
OTHER INFORMATION: "n"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1832)..(1832) stands for any nucleic acid  
OTHER INFORMATION: "n"  
US-09-281-760E-36

Query Match 30.7%; Score 179; DB 4; Length 107;  
Best Local Similarity 35.9%; Pred. No. 6.4e-14; Indels 2; Gaps 2;  
Matches 37; Conservative 22; Mismatches 42;  
Qy 7 GPSVFLPPPKPDTLMISRPEVTCVVVDVQSDPEVQFNWYDGVVHNAKTKPREEQF 66  
Db 5 GVSAYLSRPSFPD-LYVHKAPKITCLVVDLATME-GNNLTWYRESKEPVPVPLNKDHF 62  
Qy 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIK 109  
Db 63 NGTITVTSTLPVCTRDWIEGETYQCRVTHPLPKDIVRSIAKA 105

RESULT 14  
US-08-232-539D-54  
Sequence 54, Application US/08232539D  
Patent No. 5965709  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Ige Antagonists  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA: 08/178583  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 54:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-54  
Query Match 28.8%; Score 166.5; DB 2; Length 106;  
Best Local Similarity 34.3%; Pred. No. 2.1e-12; Indels 1; Gaps 1;  
Matches 35; Conservative 22; Mismatches 44;  
Qy 7 GPSVFLPPPKPDTLMISRPEVTCVVVDVQSDPEVQFNWYDGVVHNAKTKPREEQF 66  
Db 1 GVSAYLSRPSFPD-LFIRKSPITITCLVVDLATPSKGTVNLWTSRASGKPVNHSRKEEQF 59  
Qy 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIK 108  
Db 60 NGTITVTSTLPVCTRDWIEGETYQCRVTHPLPKALMRSTK 101

RESULT 15  
US-08-466-163B-1  
Sequence 1, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 1  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-466-163B-1

Query Match 26.1%; Score 152; DB 3; Length 109;  
Best Local Similarity 34.3%; Pred. No. 1.2e-10; Indels 2; Gaps 2;  
Matches 35; Conservative 21; Mismatches 44;  
Qy 7 GPSVFLPPPKPDTLMISRPEVTCVVVDVQSDPEVQFNWYDGVVHNAKTKPREEQF 66  
Db 6 GVSAYLSRPSFPD-LFIRKSPITITCLVVDLATPSKGTVNLWTSRASGKPVNHSRKEEQF 64  
Qy 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIK 108

Db 65 NGTLVTSTLPVGTQDWIEG-ETQCRVTHPHLPALMRSTTK 105

Search completed: November 17, 2005, 07:53:56  
Job time : 23.6073 secs

## SUMMARIES

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```
; Sequence 13, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-13

Query Match          96.4%; Score 562; DB 18; Length 110;
Best Local Similarity 95.5%; Pred. No. 9e-47;
Matches 105; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60

Qy 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETISKAK 110

RESULT 7
US-10-959-318-21
; Sequence 21, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG4 CH2 sequence with delta e (E268) mutation
US-10-959-318-21

Query Match          96.4%; Score 562; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 9e-47;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60
Db 1 APEFLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 60

Qy 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 PREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
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RESULT 8
US-10-267-286A-4
; Sequence 4, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:0040USCI
; CURRENT APPLICATION NUMBER: US/10/267,286A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-4

Query Match          96.2%; Score 561; DB 14; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-46;
Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 61
Db 1 PEFLLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 60

Qy 62 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 109

RESULT 9
US-10-959-318-7
; Sequence 7, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
; FILE REFERENCE: 39-302
; CURRENT APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268)
; OTHER INFORMATION: mutations
US-10-959-318-7

Query Match          96.1%; Score 560; DB 18; Length 110;
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; SEQ ID NO 12  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and e (E268)  
; OTHER INFORMATION: mutations  
US-10-959-318-12

Query Match 95.5%; Score 556.5; DB 18; Length 109;  
Best Local Similarity 96.4%; Pred. No. 3e-46;  
Matches 106; Conservative 3; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 APPVAGGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db 1 APPVA-GPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 59  
Qy 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 110  
Db 60 PREEQNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 109

RESULT 14  
US-10-959-318-17  
; Sequence 17, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: GB0324368.0  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta d (D268) mutation  
US-10-959-318-17

Query Match 93.9%; Score 547.5; DB 18; Length 109;  
Best Local Similarity 94.5%; Pred. No. 2.3e-45;  
Matches 104; Conservative 3; Mismatches 2; Indels 1; Gaps 1;  
Qy 1 APPVAGGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db 1 APPVA-GPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 59  
Qy 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 110  
Db 60 PREEQNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPAPIEKTSKTK 109

RESULT 15  
US-10-959-318-5  
; Sequence 5, Application US/10959318  
; Publication No. US20050215768A1  
; GENERAL INFORMATION:  
; APPLICANT: Armour, Kathryn L  
; TITLE OF INVENTION: Polypeptides including modified constant regions  
; FILE REFERENCE: 39-302  
; CURRENT APPLICATION NUMBER: US/10/959,318  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/004254  
; PRIOR FILING DATE: 2004-10-07

; PRIOR APPLICATION NUMBER: GB0324368.0  
; PRIOR FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta d (Q268) mutation  
US-10-959-318-5  
Query Match 93.7%; Score 546; DB 18; Length 110;  
Best Local Similarity 92.7%; Pred. No. 3.2e-45;  
Matches 102; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 APPVAGGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Db 1 APPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60  
Qy 61 PREEQFNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPSSIEKTSKAK 110  
Db 61 PREEQNSTYRVVSVLTVTLQHDWLNKGKEYCKVSNKGLPAPIEKTSKAK 110  
Search completed: November 17, 2005, 08:18:47  
Job time : 84.1279 secs

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